

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 10:09:13 ; Search time 6821 Seconds  
(without alignments)  
9941.290 Million cell updates/sec

Title: US-09-888-035A-1

Perfect score: 2330

Sequence: 1 gagaagagagttttgtagcg.....ttgaaaaaaaaaaaaaa 2330

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2313	99.3	2313	8	AB021878	AB021878 Oryza sat
2	828.8	35.6	2017	8	AY040245	AY040245 Triticum
3	793.4	34.1	2423	6	BD012814	BD012814 Gene codi
4	793.4	34.1	2423	8	AB051817	AB051817 Petunia x
5	793.4	34.1	2423	23	BD008249	BD008249 Gene codi
6	791.4	34.0	1668	6	E63046	E63046 Na+/H+ anti
7	791.4	34.0	1668	6	E63047	E63047 Na+/H+ anti
8	791.4	34.0	2637	6	AB038492	AB038492 Atriplex
9	790	33.9	2553	6	BD012815	BD012815 Gene codi
10	790	33.9	2553	8	AB051818	AB051818 Nierember
11	790	33.9	2553	23	BD008250	BD008250 Gene codi
12	777.6	33.4	2173	8	AB054979	AB054979 Ipomoea t
13	775	33.3	2135	8	AY028416	AY028416 Citrus x
14	768.8	33.0	1614	8	AF106324	AF106324 Arabidops
15	768.8	33.0	1617	8	AF510074	AF510074 Arabidops
16	768.8	33.0	1619	8	AF056190	AF056190 Arabidops
17	768.8	33.0	2218	8	AB033989	AB033989 Ipomoea n
18	768.8	33.0	2237	6	BD012802	BD012802 Gene codi
19	768.8	33.0	2237	23	BD008237	BD008237 Gene codi
20	766.8	32.9	1641	8	AF490586	AF490586 Arabidops
21	740.6	31.8	2263	8	AF370358	AF370358 Suaeda ma
22	727.8	31.2	12615	8	AP004274	AP004274 Oryza sat
23	712.4	30.6	2122	8	LES306630	LES306630 Lycopersi
24	711.8	30.5	2361	6	BD012816	BD012816 Gene codi
25	711.8	30.5	2361	8	AB051819	AB051819 Torenia h
26	711.8	30.5	2361	23	BD008251	BD008251 Gene codi
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28	508.8	21.8	1590	8	AF490588	AF490588 Arabidops
29	470.6	20.2	1677	6	AX459657	AX459657 Sequence
30	361.4	15.5	612	8	AF515632	AF515632 Cossypium
31	345.4	10.5	320	8	AF307944	AF307944 Zea mays
32	239.2	10.3	421	8	AF279671	AF279671 Mesembrya
33	202	8.7	459	8	AF279670	AF279670 Mesembrya
34	124.2	5.3	90019	8	TM021804	TM021804 Arabidops
35	119.4	5.1	116416	2	AC130801	AC130801 Medicago
36	108	4.6	93234	8	AC009465	AC009465 Arabidops
37	107	4.6	86022	8	ATAC011623	ATAC011623 Arabidops
38	101.6	4.4	139627	2	AC016779	AC016779 Oryza sat
39	97	4.2	567	11	AL772701	AL772701 Arabidops
40	96.4	4.1	2401	3	AF497828	AF497828 Caenorhab
41	96.4	4.1	2453	3	AF497829	AF497829 Caenorhab
42	96.4	4.1	7545	8	AB033990	AB033990 Ipomoea n
43	96.4	4.1	7563	8	AB055062	AB055062 Ipomoea n
44	94	4.0	132693	2	AP003543	AP003543 Oryza sat
45	94	4.0	149040	2	AP003507	AP003507 Oryza sat

ALIGNMENTS

RESULT 1

AB021878

LOCUS

Oryza sativa

AB021878

ACCESSION

VERSION

AB021878.1

GI:5731736

KEYWORDS

SOURCE

Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) cDNA

to mRNA.

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

1

Fukuda,A., Nakamura,A. and Tanaka,Y.

2313 bp mRNA linear PLN 21-MAR-2002  
Oryza sativa (japonica cultivar-group) OenHX1 mRNA, complete cds.

TITLE Molecular cloning and expression of the Na<sup>+</sup>/H<sup>+</sup> exchanger gene in  
 JOURNAL Biochim. Biophys. Acta 1446 (1-2), 149-155 (1999)  
 MEDLINE 99326147  
 REFERENCE 2 (bases 1 to 2313)  
 AUTHORS Fukuda, A., Tanaka, Y. and Nakamura, A.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-DEC-1998) Atsuneori Fukuda, National Institute of  
 Agrobiological Resources, Department of Plant Physiology, Kannondai  
 2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
 (E-mail: fukuda@abr.affrc.go.jp, Tel: 81-298-38-8376,  
 Fax: 81-298-38-8347)

## FEATURES

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1..2313  
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## polyA\_site

2313

/gene="OsNHX1"

/note="17 a nucleotides"

BASE COUNT 543 a 538 c 569 g 663 t

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Db	61	ACCAAAATCCGATTTCTCAACTGAATCCCCCCCCACGTTTCTCGTTTCAATCTGTTG	120
Qy	121	TCTCGGATCGAATCTTTGTTTCTTAATTTTACGGGAATGCGAATAGG	180
Db	121	TCTCGAATCGAATCTTTGTTTCTTAATTTTACGGGAATGCGAATAGG	180
Qy	181	CATTCAACCAACGACGAGGGAGTGGATGGTTGTTTAAAGCTCCGCATCTTGGCGG	240
Db	181	CATTCAACCAACGACGAGGGAGTGGATGGTTGTTTAAAGCTCCGCATCTTGGCGG	240
Qy	241	GAATCTCGCTCTTCTCTCGGTGGGTGCGGAGAGTCCGCCCGGTGAGGCATGG	300
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Qy	301	GGATGGAGTGGCGCGCGGTGGGGCTCTGTACACACCTCCGACTACCGGTGG	360
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RESULT 2
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LOCUS Triticum aestivum Na+/H+ antiporter (NHX1) mRNA, complete cds.
DEFINITION Triticum aestivum Na+/H+ antiporter (NHX1) mRNA, complete cds.
ACCESSION AY040245
VERSION AY040245.1 GI:15027832
KEYWORDS Triticum aestivum.
SOURCE Triticum aestivum.
ORGANISM Triticum aestivum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 2017)
Wang, Z., Zhang, J. and Chen, S.
Isolation and characterization of two Na+/H+ antiport genes from
wheat
Unpublished
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

2 (bases 1 to 2017)  
Wang, Z., Zhang, J. and Chen, S.  
Direct Submission  
Submitted (14-JUN-2001) Institute of Genetics, Chinese Academy of  
Sciences, Dacun Road 3, Beijing 100101, China  
Location/Qualifiers  
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BASE COUNT 480 a 488 c 447 g 602 t

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Best Local Similarity 71.9%; Pred. No. 2.7e-172;  
Matches 1114; Conservative 0; Mismatches 427; Indels 9; Gaps 2;

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Db 384 GCATCTTATCTTACGAGGATATTTCTTCTCATCTGCTCCGCCCATCATTTTA 443  
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 Db |||||  
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 QY 1720 TCGAGAGTACAAACCAATGTGAGGCTTCCAGGCTCCGAGTCTCTCTCCACCAAGCGA 1779  
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RESULT 3  
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 DEFINITION BD012814 2423 bp DNA linear PAT 02-AUG-2002  
 Gene coding for protein having an activity to control pH in  
 vacuoles.  
 ACCESSION BD012814  
 \* VERSION BD012814.1 GI:22093003

KEYWORDS WO 0114560-A/13.  
 SOURCE Petunia x hybrida.  
 ORGANISM Petunia x hybrida.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Petunia.  
 Iida, S., Tanaka, S. and Inagaki, Y.  
 TITLE Gene coding for protein having an activity to control pH in  
 vacuoles.  
 JOURNAL Patent: WO 0114560-A 13 01-MAR-2001;  
 SUNTORY LTD, SHIGERU IIDA, SACHIKO TANAKA, YOSHISHIGE INAGAKI  
 COMMENT OS Petunia hybrida  
 PN WO 0114560-A/13  
 PD 01-MAR-2001  
 PF 24-AUG-2000 WO 2000JP005722  
 PI 24-AUG-1999 JP 99P 236800  
 PR SHIGERU IIDA, SACHIKO TANAKA, YOSHISHIGE INAGAKI PC  
 C12N15/29, C07K14/415, C12N5/10, A01H5/00, C12P21/02 CC Nucleotide  
 sequence of DNA coding for protein having an activity to  
 CC control pH in vacuoles  
 FH Key Location/Qualifiers.  
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 /db xref="taxon:4102"  
 BASE COUNT 621 a 428 c 518 g 856 t  
 ORIGIN  
 Query Match 34.1%; Score 793.4; DB 6; Length 2423;  
 Best Local Similarity 69.9%; Pred. No. 1.8e-164;  
 Matches 1089; Conservative 0; Mismatches 461; Indels 9; Gaps 1;  
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 QY 395 CGCTGCTATCTCTCGGCCACCTCTCGAGGAGAAATCGCTGGGTCAATGAGTCCATCAC 454  
 Db |||||  
 453 GCGGTGTTATGATCGGTCTATTGTTGGAAGAAAACAGATGATGATGATGATGATGATG 512  
 QY 455 GCGCTCATCATCGGGCTCTGACCGCGGTGCTGATCTTGTGATGACCAAGGGAAGAG 514  
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 Db |||||  
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 QY 575 CTTCAATGCAAGTTTTCAGGTAAAGAAAAGCAATTTCTTCGGAATTTTCATGACGATCAC 634  
 Db |||||  
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 Db |||||  
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 QY 695 AATATTGACGAGATGAACATTTGGAACGCTGGATGTAGGAGATTTTCTTGCATTTGGAGC 754  
 Db |||||  
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 Db |||||  
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 Db 1173 TGCAATCTCACTGTGTTTCTCTGGATGCTGATGCTCACTACACCTGGCATATGT 1232  
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 Db 1353 AAGCGACAGCCCTGGAATATCAGTTTCAAGTTAGCTCAATATGCTGGTCTTGTGTTGGT 1412  
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 Db 1593 CGCAATGCAATATGATCACAGTACTATCACTGTTGCTCTTTTTCAGCAGCTGCT 1652  
 QY 1595 TGGGATGATGACAGAGCATTGATCAGGCTGCTGCTACCGC-----CTCAGGCCA 1645  
 Db 1653 TGGGTTGATGACAAACCTTTTATGATGATGATGATGATGATGATGATGATGATGATG 1712  
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RESULT 4  
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 LOCUS AB051817 2423 bp mRNA linear PLN 29-MAY-2001  
 DEFINITION Petunia x hybrida mRNA for Na H-antiporter, complete cds.  
 ACCESSION AB051817  
 VERSION AB051817.1 GI:14211573  
 KEYWORDS

## SOURCE

ORGANISM

Petunia x hybrida cDNA to mRNA.

Petunia x hybrida

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Petunia.

## REFERENCE

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Db 1609 COTTTGTCCCGGTTTCACTTACTGAACAAGC 1641

RESULT 7
E63047 Na+/H+ antiporter protein and gene encoding it. linear PAT 31-JAN-2002
LOCUS E63047
DEFINITION E63047
ACCESSION E63047
VERSION E63047.1 GI:18628472
KEYWORDS JP 2000157287-A/2.
SOURCE unidentifed.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1668)
AUTHORS Shono,M., Hayakawa,T. and Tanaka,A.
TITLE Na+/H+ antiporter protein and gene encoding it
JOURNAL Patent: JP 2000157287-A 2 13-JUN-2000;
COMMENT PLANTECH RESEARCH INSTITUTE
OS Atliplex gmelini
PN JP 2000157287-A/2
PD 13-JUN-2000
PF 16-SEP-1999 JP 1999261606
PR
PI MARIKO SHONO,TAKAHIKO HAYAKAWA,AKIRA TANAKA
PC C12N15/09,A01H5/00,C07K14/415,C12Q1/68//C12N5/10,C12N15/00, PC
C12N5/00
CC Key Location/Qualifiers
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FT /organism='Atliplex gmelini'.

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source Location/Qualifiers
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/organism='unidentified'
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BASE COUNT 397 a 342 c 376 g 553 t
ORIGIN

Query Match 34.0%; Score 791.4; DB 6; Length 1668;
Best Local Similarity 70.0%; Pred.No. 4.8e-164;
Matches 1115; Conservative 0; Mismatches 436; Indels 42; Gaps 2;

QY 339 ACGACCTCCGACTACGGCTCGGTGTGCCATCAACCTGTTGTCGCGCTGCTCTCGGCC 398
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Db 109 TGTATCTAAATTTGGTCTATCTTTAGAGGAGAAATCGTTGGATGAATGATCCATCCTGCC 168
QY 459 CTCTATCTCGGGCTCTGCACCGGCTGTGATCTTGTGTGATGACCAAGGAAAGAGCTCG 518
Db 169 CTTCTTATAGTTTGGCTACTGGGGTTGTGATTTCTGTGATTTAGTGGAGGAAAGTTCA 228
QY 519 CACTTATTCGTTTCAGTGAGGATCTCTTCTTCACTACCTCTCTCTCTCTCTCTCTCT 578
Db 229 CATCTTTTGTGCTTTCAGTGAAGATCTTTTCTTCAATACCTTCTTCCACCGATTATTC 288
QY 579 AATCAGGTTTTCAGGTAAAGAAAGCAATTTCTTCGGATTTTCATGACCATCACATTA 638
Db 289 AATCAGGCTTTTCAGGTGAAGAAAGCAATTTCTTCGGCAACTTCTTCTTCTTCTTCT 348
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QY 639 TTTGGAGCGTGGGACAAATGATATCTTTTTCACAAATATCTATGTGCTGCAATTGCAATA 698  
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Db 409 TTTTAAAGAAATTTGGATAATTTGGTACTCTGGAGTTGGCAGACTATCTTGCAATTTGGTGAATA 468  
QY 759 TTTTCTCGGACAGATTTCTGTCTGACAAATTTGAGGCTCTCAATCAGGATGAGACACCTTTT 818  
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QY 819 TTTGACAGTCTGTGATTTGCTGGAAGGTTTGTGGAACGATCTCAATCAATTTGCTTTTTC 878  
Db 529 CTCTACAGTCTGTGCTTTTGGGAGGTTTGTGGAACGATCTCAATCAATTTGCTTTTTC 588  
QY 879 AACGCACCTACAGAACTTTGATCTTGTCCACATAGATCGGCTGCTGTTCTGAAATCTTGT 938  
Db 589 AATGCAATTCAGAGCTTTGACCTCACAAGAAATGATCACAGAAATGATCTTACAAATTTATG 648  
QY 939 GGGAACTCTTTTATTTATTTTTCGAGACCTTCTCTGGAGTATTTGCTGGAATGCTC 998  
Db 649 GGCACACTCTTATATTTATTTATCGCAAGCAGATCTCTGGAGCAATTTACTGCTTGCCTC 708  
QY 999 AGTCATACATAATCAAGAGCTATACATTTGGAAGGATCTCTACTGACCGTGGAGTTGCC 1058  
Db 709 AGTGTACATATTCAAAGAGCTGACTTTTGAAGGATCTTCCACTGATCTGAGTTGCT 768  
QY 1059 CTTATGATGCTCATGGCTTACCTTTTCATATATGCTGCTGAGTTGCTGATTTGAGCGGC 1118  
Db 769 TTAATGATGCTTATGGCTTATCTATCTTACATGCTGCTGAACTTTTCTATTTGAGTGA 828  
QY 1119 ATTCTCACCGTATTTCTGTTGTTATGTTATGTTACATTTACATCTTGGCATAGCTCACA 1178  
Db 829 ATTCTTACTGTTATTTCTGTTGGGATGTTGATGTTCCCATTTATACCTGGCAATGTCACA 888  
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Db 889 GAGAGCTCAAGAGTTTACAAAGAGCAGCATTTTTCACACATCTCTTGTGCTGAGTT 948  
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QY 1359 AGAGCTGCTTTTGTATTTCCCGCTGCTGTTCTTTGTCGAACCTTAAACAAAGAGCAGCAAT 1418  
Db 1069 AGAGCAGCTTTTGTATTTTCCCTTATCTGTTGATGATGATGATGATGATGATGATGATGAT 1128  
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QY 1599 ATGATGACAAAGCCTATGATAGGCTGCTGCTACCGGCTCAGGCACTCTGTCACCTCT 1658  
Db 1309 TTGCTGACAAAGCCTCTCATCATGTTTCTGCTGCTCAACGAAACACTTCACTAGTTGC 1368  
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Db 1369 AGCACCGTATCATGATGTTGGGAAGTCCAAAGTCATCTGTTGCCACTCTCTTGGAGGCAAC 1428

QY 1707 CAAGTTCTGACCTCGAGGATACAC-----AAC 1736  
Db 1429 CAAGATTATGAATGTGTGGAAACCGAAACCATGAGACACCACTGAGCGCGACT 1488  
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DEFINITION cds.  
ACCESSION AB038492  
VERSION AB038492.1 GI:9857313  
KEYWORDS Na/H antiporter Nhx1.  
SOURCE Atriplex gmelini cDNA to mRNA.  
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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1  
Hameda, A., Shono, M., Xia, T., Ohta, M., Hayaashi, Y., Tanaka, A. and  
Hayaashi, T.  
Isolation and characterization of a Na<sup>+</sup>/H<sup>+</sup> antiporter gene from the  
halophyte Atriplex gmelini  
Plant Mol. Biol. 46 (1), 35-42 (2001)  
21330247  
2 (bases 1 to 2637)  
Hayaashi, T., Hameda, A. and Tanaka, A.  
Direct Submission  
Submitted (17-FEB-2000) Takahiko Hayaashi, Plantech Research  
Institute, Research Center, 1000 Kamoshida-cho, Aoba-ku, Yokohama,  
Kanagawa 227-0033, Japan (E-mail: pri0012@cc.m-kagaku.co.jp,  
Tel:+81-45-963-3520, Fax:+81-45-962-7492)  
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Query Match 34.0%; Score 791.4; DB 8; Length 2637;

Best Local Similarity 70.0%; Pred. No. 4.9e-164;  
Matches 1115; Conservative 0; Mismatches 436; Indels 2;

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RESULT 9  
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LOCUS  
DEFINITION Gene coding for protein having an activity to control pH in vacuoles.  
ACCESSION BD012815  
VERSION BD012815.1 GI:220933004  
KEYWORDS WO 0114560-A/14.  
SOURCE unidentified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 2553)  
AUTHORS Iida S., Tanaka, S. and Inagaki, Y.  
TITLE Gene coding for protein having an activity to control pH in vacuoles  
JOURNAL Patent: WO 0114560-A 14 01-MAR-2001;  
SUNTORY LTD, SHIGERU IIDA, SACHIKO TANAKA, YOSHISHIGE INAGAKI  
COMMENT OS Nierembergia hybrida  
PN WO 0114560-A/14  
PD 01-MAR-2001  
PF 24-AUG-2000 WO 2000JP005722  
PR 24-AUG-1999 JP 99P 236800  
PI SHIGERU IIDA, SACHIKO TANAKA, YOSHISHIGE INAGAKI PC  
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sequence of DNA coding for protein having an activity to

CC control pH in vacuoles  
CC Key Location/Qualifiers.  
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Nierembergia caerulea cDNA to mRNA.			
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
Asteridae; euasterids I; Solanales; Solanaceae; Nierembergia.			
1 (sites)			
Iida,S., Kusumi,T., Yonekura-Sakakibara,K. and Tanaka,Y.			
Plant Na-H antiporter			
Unpublished			
2 (bases 1 to 2553)			
Tanaka,Y., Yonekura-Sakakibara,K., Kusumi,T. and Iida,S.			
Direct Submission			
Submitted (27-NOV-2000) Yoshikazu Tanaka, Suntory Ltd., Institut			
for Fundamental Research; Wakayama-dai, 1-1-1, Mishima, Shimam			
Osaka 618-8503, Japan (E-mail:Yoshikazu_Tanaka@suntory.co.jp,			
Tel:81-75-962-8807, Fax:81-75-962-8262)			
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DB	2016	TCAACCCCATCTCACACGGTACATTACTACTGGAGAAAATTTGACATGCAATTCATGCT	2075
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DB	2076	CCTGTTTTCGGTGGAGGTTTGTACCTTTTGTTCAGGATCACCTTACTGAAACCGGTC	2135
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RESULT 11

BD008250

ID BD008250 standard; DNA; UNC; 2553 BP.

XX AC BD008250;

XX AC BD008250.1

SV BD008250.1

XX DT 08-FEB-2002 (Rel. 70, Created)

DT 08-FEB-2002 (Rel. 70, Last updated, Version 1)

XX DE Gene coding for protein having an activity to control pH in vacuoles.

XX KW JP 03075543-T/14.

XX OS unidentified

XX OC unclassified.

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RP 1-2553  
PA Iida S., Tanaka S., Inagaki Y.;  
RL "Gene coding for protein having an activity to control pH in vacuoles";  
RL Patent number JP03075543-T/14, 23-FEB-2001.  
RL SUNTORY LTD, SHIGERU IIDA, SACHIKO TANAKA, YOSHISHIGE INAGAKI.  
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CC PR 24-AUG-1999 JP 99P 236800  
CC PI SHIGERU IIDA, SACHIKO TANAKA, YOSHISHIGE INAGAKI  
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Best Local Similarity 69.7%; Pred. No. 1e-163;  
Matches 1088; Conservative 0; Mismatches 465; Indels 9; Gaps 1;  
  
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QY 939 GGGAACTTCTTTTATTTTGTGCGAGCACTTCTCTTGGAGTATTTGCTGGATTTGCTC 998

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QY 1059 CTTATGATGCTCATGCTTACCTTTTCAATATGCTGCTGAGTGTCTGATATTTGAGCGGC 1118  
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DB 1416 GAGAGCTCAAGAGTCACTACCAAGCACAGTTTGTACATTTATTTGCTGAATA 1475  
QY 1239 TTTCTCTCTCTATGTTGGGATGATGATTTGGATATTTGAAATTTGGAGTTGCCAGT 1298  
DB 1476 TTTCAATTTCTTTATGTTGATGATGCTTTTGGACATTTGAGAGTGAAGTTTGAAGC 1535  
QY 1299 GACAGACCTGGCAATTCGATTTGGGATAGCTCAATTTTGTAGGATTTGTTCTGATTGA 1358  
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QY 1359 AGAGCTGCTTTTGTATTTCCCGCTGTCTTGTGTCGAACCTTAACAAAGAACGACCGAAT 1418  
DB 1596 AGGGAGCCTTTGTTTCCCTTGTCTTGTCTTGTCCACTTGTCCACCAAGAAATCCTGAG 1655  
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QY 1890 CA 1891  
DB 2136 GA 2137

RESULT 12  
AB054979  
LOCUS  
DEFINITION  
ACCESSION

AB054979 2173 bp mRNA linear  
Iponomea tricolor ItNHX1 mRNA for Na+/H+ exchanger, complete cds.  
AB054979

VERSION	AB054979.1	GI:14488269	
KEYWORDS	Ipomoea tricolor cDNA to mRNA.		
SOURCE	Ipomoea tricolor		
ORGANISM	Ipomoea tricolor		
REFERENCE	Ipomoea tricolor cDNA to mRNA.		
AUTHORS	Yonekura-Sakakibara K., Tanaka Y., Kusumi T. and Iida S.		
TITLE	Genes encoding the vacuolar Na <sup>+</sup> /H <sup>+</sup> exchanger and flower coloration		
JOURNAL	Plant Cell Physiol. 42 (5), 451-461 (2001)		
MEDLINE	21276661		
REFERENCE	2 (bases 1 to 2173)		
AUTHORS	Fukada-Tanaka, S., Inagaki, Y., Yamaguchi, T. and Iida, S.		
TITLE	Submitted (23-JAN-2001) Sachiko Fukada-Tanaka, National Institute		
JOURNAL	for Basic Biology, Division of Gene Expression and Regulation 1;		
	Myodaiji-cho, Okazaki, Aichi 444-8585, Japan		
	(E-mail: sachiko@nibb.ac.jp, Tel: 81-564-55-7682, Fax: 81-564-55-7685)		
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ORIGIN			
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Qy	402	ATCGTCCTCGGCACCTCCTCGAGGAGATCGCTGGGTCAATGAGTCCATCACCGCGCTC	461
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Qy	462	ATCATCGGGCTCTGCACCGCGGTGTGTGATCTTGTGTGATGACCAAGGAGGAGTCCGAC	521
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Qy	762	TCTGGACAGATTTCTGTCTGCACATTGAGGTCTCAATCAGGATGAGACACCCCTTTTG	821
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Qy	882	GCATACAGAACTTTGATCTTGTCCACATAGATCGGCTGTCTGTCTCAAAATTTCTTGGG	941
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Db	1573	GCAATAATGATCAAGTACTGTGTTTACGGTGTCTGTTTGTTCAGCACAGTTGTTATCGGGTTG	1632
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		FFCGIVSHVTHNVNVTSSRTTTHKHTATLSFLAETFIPLYVGMADLIDIKWRSVST	
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AF510074 1617 bp mRNA linear PLN 23-MAY-2002

LOCUS  
AF510074  
DEFINITION  
Arabidopsis thaliana Na<sup>+</sup>/H<sup>+</sup> antiporter (NHX1) mRNA, complete cds.

ACCESSION  
AF510074  
VERSION  
AF510074.1 GI:21105719

KEYWORDS  
Arabidopsis thaliana.

SOURCE  
Arabidopsis thaliana.

ORGANISM  
Arabidopsis thaliana.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eudesids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 1617)

REFERENCE  
Baek S.H.  
Isolation and characterization of a Na<sup>+</sup>/H<sup>+</sup> antiporter gene from  
Arabidopsis  
Unpublished  
2 (bases 1 to 1617)

REFERENCE  
Baek S.H., Kim H.S., Lee Y.T., Lee M.H. and Yun S.J.  
Direct Submission  
Submitted (07-MAY-2002) Rice Research Division, National Honam  
Agricultural Experiment Station, Songhak-dong, Iksan, Jeonbuk  
570-080, Republic of Korea



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 10:03:13 ; Search time 541 Seconds  
(without alignments)  
9698.995 Million cell updates/sec

Title: US-09-888-035A-1

Perfect score: 2330

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 segs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	790	33.9	2553	22	AAF75765
5	768.8	33.0	2178	20	AAZ22591
6	768.8	33.0	2237	22	AAF75752
7	746.8	32.1	2284	20	AAZ22595
8	711.8	30.5	2361	22	AAF75766
9	508.8	21.8	1788	20	AAZ22592
10	482.8	20.7	1674	24	ABK12638
11	340.4	14.6	378	20	AAZ22606
12	139.2	6.0	330	20	AAZ22611
13	138.8	6.0	281	24	ABL73323
14	109.4	4.7	1824	21	AAC95372
15	109.4	4.7	1824	21	AAC95373
16	109.4	4.7	2080	21	AAC95370
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25	64.2	2.8	2617	23	ABL17669
26	64	2.7	5597	22	AAH98721
27	62.6	2.7	2584	18	AAZ51330
28	62.6	2.7	2584	23	AAZ92733
29	59.8	2.6	7778	23	ABL17668
30	58.4	2.5	4408	24	ABL61776
31	58.4	2.5	4598	24	ABK35727
32	52.4	2.2	1354	22	AAF97931
33	52.4	2.2	4794	23	AAZ94071
34	51.8	2.2	1964	23	ABL03375
35	51.4	2.2	2890	24	AAZ44679
36	47	2.0	714	20	AAZ22593
37	47	2.0	2122	20	AAZ22603
38	46.8	2.0	263	21	AAZ44056
39	46.4	2.0	2753	22	AAZ02660
40	44.6	1.9	1536	23	AAZ575121
41	44.6	1.9	3489	21	AAA30290
42	44.6	1.9	3489	22	AAF82901
43	44.6	1.9	3489	24	ABA93487
44	44.6	1.9	32207	20	AAV73805
45	44.6	1.9	137507	19	AAV19941

#### ALIGNMENTS

#### RESULT 1

AAA61876  
ID AAA61876 standard; cDNA; 2330 BP.

XX AC AAA61876;

XX DT 07-NOV-2000 (first entry)

XX DE cDNA encoding rice Na<sup>+</sup>/H<sup>+</sup> antiporter, OsNHX1.

XX KW OsNHX1; Na<sup>+</sup>/H<sup>+</sup> antiporter; sodium/proton antiporter; countertransporter;

XX KW active transport; rice; transgenic plant; salt-tolerance; ss.

XX OS Oryza sativa.

XX FH Key Location/Qualifiers

XX FT CDS 297..1904

XX FT /\*tag= a

XX FT /product= "Rice Na<sup>+</sup>/H<sup>+</sup> antiporter"

XX PN WO200037644-A1.

XX PD 29-JUN-2000.

XX PF 22-DEC-1999; 99WO-JP07224.

XX PR 22-DEC-1998; 98JP-0365604.

XX PA (NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES.

XX PI Fukuda A, Tanaka Y;

DNA encoding Physc  
Rice Na<sup>+</sup>/H<sup>+</sup> antiporter  
Arabidopsis Na<sup>+</sup>/H<sup>+</sup> a  
Corn tassell-derive  
Cat flea HMT Na/H  
Cat flea HMT Na/H  
Cat flea HMT Na/H  
Cat flea HMT Na/H  
Rice Na<sup>+</sup>/H<sup>+</sup> antiporter  
Drosophila melanog  
Human transporter  
Arabidopsis thalia  
Human secreted pro  
Human transporter  
Human secreted pro  
Drosophila melanog  
Human EST-derived  
Human Na<sup>+</sup>/H<sup>+</sup> excha  
DNA encoding novel  
Drosophila melanog  
Colon adenocarcino  
cDNA sequence #118  
Human secreted pro  
DNA encoding novel  
Drosophila melanog  
Human transporter  
Arabidopsis thalia  
Arabidopsis thalia  
Human secreted exp  
Human secreted pro  
DNA encoding novel  
Kaposi's sarcoma-a  
Nucleotide sequenc  
Kaposi's sarcoma-a  
KSHV LUR DNA (nucl  
KSHV long unique c









Db 949 TTCCTATTTCTATATGTCGGTATGCAATGGAATGGAATGTTGTTAGT 1008  
Qy 1299 GACAGACTGGCAATCAATTTGGGTAAGCTCAATTTTGTAGGATGTTCTGATTGGA 1358  
Db 1009 GATAGTCTGGCATTTCTGTGCTGAGTTCATATTTGTAGTCTAGTCATGTTGGA 1068  
Qy 1359 AGAGCTGTTTGTATTTCCGCTGCTGTTCTTGTGCAACCTAAACAAAGAGGACCGAAT 1418  
Db 1069 AGAGCAGCTTTTGTATTTCCCTTATCTGTTGTTGATGAATTTGCCAAGAAATCGCAAGT 1128  
Qy 1419 GAAAAATTAACCTGGAGACAGCAAGTTGTAATATGTTGGCTGGCTGATGAGAGGACT 1478  
Db 1129 GAAAAAGTCACTTTCAACAGCAGATTTGATATGTTGGCTGTTGTTATGAGAGTGTCT 1188  
Qy 1479 GTGTGCAATGCTTGTGTTTACAAAGTTTACAAAGTCTGGCCATCTCAGCTGCAAGC 1538  
Db 1189 GTTTCATGGCACTTGTATTAATCAGTTTACGAGGTCTGGGCACACAGCTTAGGGGA 1248  
Qy 1539 AATGCAATATGATCACAGCACCATCACTGCTGTTCTTTTATGACTATGTTGTTGGG 1598  
Db 1249 AATGCAATCATGATCACAGCACCATCACTGCTGTTCTTTTATGACTATGTTGTTGGG 1308  
Qy 1599 ATGATGCAAAAGCATTGATCAGCTGCTGCTACCGGCTCAGGCCATCTGTCACCTCT 1658  
Db 1309 TTGCTGCAAAAGCCTCTCATCATGTTTGTGCTCTCAACCGAACAACCTTCACTAGTGC 1368  
Qy 1659 GAGCCTTCTATCA-----CCAAAGTCCCTGCAATCTCTCTCTGACACAGCATG 1706  
Db 1369 AGCAGGTATCAGATGTTGGGAGTCCAAAGTTCATACTGTTGCCATCTCTTGGAGGCAAC 1428  
Qy 1707 CAAGGTTCTGACCTCGAGAGTACAAAC-----AAC 1736  
Db 1429 CAAGATTATGAAGTTGATGTTGGGAAACCGAAACCATGAAGACACCACTGAGCGCGGACT 1488  
Qy 1737 ATTGTGAGGCTTCCAGCTCGGATGCTCTCTACCAAGCGGACCACTGCTCCACTAC 1796  
Db 1489 ATAGTTCGACCTAGTACGCTCCGATGCTTCTAAATGCACTACTCACCGCTCCATCAC 1548  
Qy 1797 TACTGGCGCAAGTTTCGAGCGCTGATGCGACCGATGTTTGGCGGCGCGGTTCTGCTG 1856  
Db 1549 TATTGGCGCAATTCGATGACTCTCTCTATGCGGCGCGGTTTGTGCGCGGTTTGTGA 1608  
Qy 1857 CCCTTCTCCCTGGATCAACCAACCGAGCAGC 1889  
Db 1609 CTTTGTGCGCGGTTTCACTACTACTGAAACAAAGC 1641

## RESULT 4

AAF75765  
ID AAF75765 standard; DNA; 2553 BP.

AC AAF75765;

DT 14-MAY-2001 (first entry)

XX Gene regulating the pH of vacuoles.

XX Vacuole pH regulation; flower colour; ds.

XX Nierenbergia hybrida.

XX WO200114560-A1.

XX 01-MAR-2001.

XX 24-AUG-2000; 2000MO-JP05722.

XX 24-AUG-1999; 99JP-0236800.

XX (SUNR) SUNTORY LTD.

XX Iida S, Tanaka S, Inagaki Y;

XX

DR WPI; 2001-191648/19.  
DR P-PSDB; AAB73253.

XX Morning glory-originated gene encoding a protein with pH regulation  
PT activity in vacuoles, useful in controlling flower color to give new  
PT breeds of colorful plants for cut flowers, particularly applicable in  
PT horticulture -

PS Example 7; Page 45-49; 68pp; Japanese.

XX The present sequence is a gene, which encodes a protein with vacuolar pH  
CC regulatory activities. The gene enables flower colour to be controlled  
CC via regulation of the vacuolar pH, colours can range from blue to red in  
CC colour spectrum. The gene is useful in controlling flower colour to give  
CC new breeds of colourful plants for cut flowers, particularly applicable  
CC in horticulture.

XX Sequence 2553 BP; 666 A; 487 C; 535 G; 865 T; 0 other;

Query Match 33.9%; Score 790; DB 22; Length 2553;  
Best Local Similarity 69.7%; Pred. No. 9.1e-208;  
Matches 1088; Conservative 0; Mismatches 465; Indels 9; Gaps 1;

Qy 339 ACAGCTCCGACTACGCTGCTGCTGCTCCATCAACCTGTTGCTGCGCTGCTCTCGGCC 398

Db 576 ACAACTTCTGATCATCAATCAATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 635

Qy 399 TCACTGCTCTCGGCACCTCTCGAGGAGATCGCTGGTCAATGAGTCCATCAACCGCG 458

Db 636 TGATTTGATCGCTCATTTATTGAGGAGAAACAGATGATGATGATGATGATGATGATG 695

Qy 459 CTCATCATCGGCTCTGCACCGCGCTGCTGCTGCTGATGACCAAGGAGGAGCTGCG 518

Db 696 CTTGTGATTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 755

Qy 519 CACTTATTCGCTTCACTGAGGATCTCTTCTCATCTACCTCTCCCTCCGATCATCTTC 578

Db 756 CATATTTAGTCTCAGCGAAGATCTTTTCTTCAATTAACCTCTTCCACCGATCATTTT 815

Qy 579 AATGAGGTTTTCAGTAAAGAAAGCAATTTCTCCGAAATTTTCATGACGATCATTTA 638

Db 816 AATGCTGGGTTTCAGTGAAAGAAATCAATTTCTCCGCAATTTTCAGTACTATGCTC 875

Qy 639 TTTGAGCGCTCGGACATGATATCTCTTTTTCACAAATATCTATTTGCTGCCATTCGA 698

Db 876 TTTGGGCGATTTGGCACCTTGTATATCGTTTCAATTTATATATCAGCGGCTGCTAT 935

Qy 699 TTCAGCAAGTGAACATTTGGAACGCTGATGATGATGATGATGATGATGATGATGATG 758

Db 936 TTTCAAGAAATGGATATTGGACACCTTGAATTTGGAGATTTACCTTTGCAATTTGG 995

Qy 759 TTTTCTGCGACAGATTTCTGCTGACATTTGAGGCTCTCAATCAGATGAGACACCTTT 818

Db 996 TTTGCTGCAACAGATTTCTGATGACCTTACAGTGTCTTAATCAGAGAAACACCGTTA 1055

Qy 819 TTGTACAGTCTGATTTCCGTTGAAGGTGTTGTAACAGTGTGATGATGATGATGATG 878

Db 1056 TTGTACAGTCTAGTGTGTTGGAGAAGGTGTTGTAATGATGATGATGATGATGATG 1115

Qy 879 AACGCACTACAGAACTTTGATCTTGTCCACATAGATGCGGCTGCTGCTGCTGCTGCT 938

Db 1116 AATGCTGCTCAGAACTTTGACTTATCTCATATCAGACAGGCAAGCTCTGCAATTA 1175

Qy 939 GGGAACTCTCTTTTATTTATTTTGTGAGCACCCTTCTTGGAGTATTTGCTGATGCTC 998

Db 1176 GGAACCTTTCTATATCTGTTTCCCTCGAGCACTTTTCTAGGGGTGCTGTTGCGCTACT 1235

Qy 999 AGTGATACATAATCAAGAGCTATACATTTGGAAGGCAATTTCTACTGACCGGTGCTGC 1058

Db 1236 AGTGCCCTTTTATTAAGAACTCTACTTTTGAAGGCACTCGACTGATGCTGAGGTGCT 1295

Qy 1059 CTTATGATGCTCATGGCTTACCTTTCAATATATGCTGGCTGATGCTGATGCTGATG 1118













XX 18-JAN-2000 (first entry)  
 DT Arabidopsis thaliana Na/H transporter gene AtNHX2.  
 DE  
 XX Sodium; proton; antiport; transporter; salt tolerance; salt management;  
 KW transgenic plant; survival; soil; farming; accumulation; irrigation;  
 KW crop; ss.  
 XX Arabidopsis thaliana.  
 OS  
 XX WO9947679-A2.  
 PN  
 XX 23-SEP-1999.  
 PD  
 XX 18-MAR-1999; 99WO-CA00219.  
 PF  
 XX 18-MAR-1998; 98US-0078474.  
 PR 15-JAN-1999; 99US-0116111.  
 PR  
 XX (BLUM/) BLUMWALD E.  
 PA (APSE/) APSE M.  
 PA (SNED/) SNEDDEN W.  
 PA (AHAR/) AHARON G.  
 XX  
 PI Blumwald E, Apse M, Snedden W, Aharon G;  
 XX  
 XX WPI: 1999-571840/48.  
 DR P-PSDB; AAY40902.  
 DR  
 XX Nucleic acid molecules encoding sodium/proton transport polypeptides,  
 PT useful in genetic engineering salt tolerance in crop plants -  
 PT  
 XX Claim 4; Fig 1B; 93pp; English.  
 PS  
 XX The invention relates to an isolated nucleic acid molecule encoding a  
 CC plant Na/H antiport (PNHX) transporter polypeptide, or a fragment and  
 CC capable of increasing salt tolerance in a cell. This sequence corresponds  
 CC to the gene encoding the AtNHX2 transporter from Arabidopsis thaliana.  
 CC The Na/H transporter polypeptides provide a means of intracellular salt  
 CC management, particularly in plants. The sequences are useful for  
 CC producing transgenic plants that are capable of surviving in soil with  
 CC high salt levels that would normally inhibit growth of the crop species.  
 CC This would be useful in farming land in areas that are generally  
 CC considered unproductive through salt accumulation and poor irrigation,  
 CC e.g. in India, Australia, and prairies in USA or Canada. Commercial  
 CC crops, such as potatoes, tomatoes, brassica, cotton, sunflower,  
 CC strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley,  
 CC atriplex, sorghum, alfalfa, salicornia and others would benefit from  
 CC increased salt tolerance.  
 XX  
 SQ Sequence 1788 BP; 475 A; 367 C; 370 G; 576 T; 0 other;

Query Match 21.8%; Score 508.8; DB 20; Length 1788;  
 Best Local Similarity 62.7%; Pred. No. 5.2e-130;  
 Matches 811; Conservative 0; Mismatches 477; Indels 6; Gaps 1;

QY 346 CCGACTACGGCTGGTGGTCCATCAACCTGTTTCGTGGCGCTGCTCGCGCTGATCG 405  
 DB 104 CTGAGCATCTCAGTGATACCAATCTCAGTGTTTCATCGGCATTCCTGCTAATTAG 163  
 QY 406 TCCTCGGCACCTCCTCGAGGAGATCGTGGGTCAATGAGTCCATCCCGCGCTCATCA 465  
 DB 164 TTATCGGCCACTTGCTTGAAGAGAATCGATGGGTTAATGAATCTATTACCGCCATTTAG 223  
 QY 466 TCGGCTCGCACCGCGGTGGTGTGATCTTGCTGATGACCAAGGAGGAGCTCGCACTAT 525  
 DB 224 TAGGAGCAGCATCAGGAACAGTGTATCTTACTTATAGTAAAGGAAAAGTTTCATATTT 283  
 QY 526 TCGTCTTCAGTGAGGATCTCTTCTTCATCTACCTCCCTCCGATCATCTTCAATCAG 585  
 DB 284 TGGTGTGGATGAGAACTCTCTTCATTTACCTTCTTCCCAATTAATCTTCAATGCTG 343

QY 586 GTTTTCAGGTAAGAAAAGCAATTTCTTCGGAAATTTTCATGACCATCACATATTTCGAG 645  
 DB 344 GGTTCCAAGTTAAGAAAAGAAAGTTTTTTCACAACTTTTAAACCATCATGTGCTTTGGTG 403  
 QY 646 CCGTCGGGACAAATGATATCTCTTTTTCACAAATATATATGCTGCCAATTCGAATATTCAGCA 705  
 DB 404 TGATTGGAGTTTTCATCTCCACTGCTCATTAATCTCTGTTGGGACTTGGTGGCTGTTCCCA 463  
 QY 706 GAATGACAACTTGGAAACGCTGGATGTAGGAGATTTTCTTGGCAATTTGGAGCCATCTTTTCTG 765  
 DB 464 AGTTGGGATTTAAGGGGTTGAGTGCTAGAGACTATCTGCCATAGGAACGATTTTCTCAT 523  
 QY 766 CGACAGATTCGTCTGTCGACATTCGAGGTCCTCAATCAGGATGACACACCCCTTTTGTACA 825  
 DB 524 CAACCTGATACCTGTTGCACTCTACAGATTTCCCATCAAGATGAACACCATTTGCTATACA 583  
 QY 826 GTCTGGTATTCGGTGAAGGTGTGTGAACGATGCTATCAATCAATTTGTCTTTTCAACGCAC 885  
 DB 584 GCTTAGTCTTTGGAGAGGAGTGGTGAATGATGCAACCTCAGTTGTACTGTTCAACGCCG 643  
 QY 886 TACGAACTTTGATCTTGTCCACATAGATCGGCTGTGCTTCTGAAATTTCTTGGGGAAT 945  
 DB 644 TGCAAAAGATTCAAATTTGAAAAGCCTAACCGGTTGGACGGCGCTGCAAGTATTTGGGAAT 703  
 QY 946 TCTTTTATTTATTTTGTGAGACCTTCTTGGAGTATTTGCTGGATTTGCTGGATGCTCAGTGCA 1005  
 DB 704 TTTCTGACCTCTCTCTCAACAAGCACACTTCTCGGAATTTGGTGGGGCTAATAACATCTT 763  
 QY 1006 ACATAATCAAGAAGCTATACATTTGGAAGGCATTTCTACTGACCGTGGAGTTGCCCTTATGA 1065  
 DB 764 TTGTTCTTTAAACCTTGTTATTTTGGAGACATTTCTACTACAGCGAATCTGCCATCAAG 823  
 QY 1066 TGCTCATGGCTTACCTTTTCATATATGCTGGCTGAGTTGCTAGATTTTGAGCGGCAATTTCTCA 1125  
 DB 824 TTCTAATGGCTTACCTTTTCATATATGTTGGCTGAGCTCTTCTCATTAAGTGAATTTCTTA 883  
 QY 1126 CGGTATTTCTTGTTGGTATTTGTAATGTCACATTAACCTTGGCATAACCTCACAGAGTT 1185  
 DB 884 CTGTTTTCTTCTGTTGGTGTGTTTAAATGTGCGCATTTGCAATATACATTAACGTGACAGAGCT 943  
 QY 1186 CAAGAGTTTACAAACAAAGCAGCATTTGCAACTCTGCTCTTCAATTCCTGAGACTTTTCTCT 1245  
 DB 944 CAAGAATCACTTCCAGGATGTTATTTGCAATGTTGCTCTTTTATTCGGGAGACATTCATAT 1003  
 QY 1246 TCTCTGATTTGGGATGGATGCAATTTGGATATTTGAAATATGGAGTTTCCAGTGCACAGAC 1305  
 DB 1004 TTCTGATGTTGGAACAGATGCTCTTGATTTTACAAAGTGAAGACAAGCAGCTTAAGCT 1063  
 QY 1306 CTGGCAATTCATTCGGGATAGCTCAATTTTGTAGGATTTGTTCTGATTTGGAAGAGCTG 1365  
 DB 1064 TTGGGGGTACTCTGGGTGTCTCCGGTGCATAAACCGCATTTAGTATTTGCTTGGACGAGCAG 1123  
 QY 1366 CTTTGTATTTCCGCTGTCTGTTCTTTCGAACTTAAACAAAG-----GCACCGAATG 1419  
 DB 1124 CATTTGTCTTTCATCTCTCGGCTTAAACAAATTCATGAACGAGCACACTGAAAGAACG 1183  
 QY 1420 AAAAAATAAACCCTGGAGACAGCAAGTTGTAATATGTTGGCTGGGCTGATGAGAGAGCTG 1479  
 DB 1184 AGTCTATCACATTTAAGCATCAGGTGATCATTTGGTGGGCGAGTCTAATTCGAGGTGCTG 1243  
 QY 1480 TGTGATTTGCTCTTCTTACATTAAGTTTACAAAGATCTTGGCCATCTCAGCTGCACGCA 1539  
 DB 1244 TCTCAATGCTCTGGCTTTCAAGCAGTTTACATATCCGGTGTTCATATTGGATCTCTGGA 1303  
 QY 1540 ATGCAATATGATCACAGCACCATCATCTGTTCTTTTATAGCACTATGGTATTTGGGA 1599  
 DB 1304 ATGCTGCCATGTCACCAACACCATATCTGTTGTTCTCTTTACTACACTGGTCTTTGGTT 1363  
 QY 1600 TGATGACAAAGCCATTTGATTCAGGCTGCTGCTACC 1633  
 DB 1364 TCTCTCAAAACCACTTGTGAATTTATCTCTCTCC 1397

RESULT 10  
ID ABK12638 standard; cDNA; 1674 BP.  
AC ABK12638;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE DNA encoding Physcomitrella patens Na<sup>+</sup>/H<sup>+</sup> antiporter PpNHX1.  
XX  
KW Plant; Na<sup>+</sup>/H<sup>+</sup> antiporter; PpNHX1; expressed sequence tag; EST; gene;  
KW plant protectant; cytosolic; stress tolerance; plant defence activity;  
KW canker; gall; tumour; appressorium; pathogenic stress; herbicide;  
KW insecticide; acid rain; drought tolerance; plant hormone synthesis;  
KW ultraviolet tolerance; flower development; terpene synthesis;  
KW plant organoleptic; ss.  
XX  
OS Physcomitrella patens.  
XX  
PN WO200216423-A2.  
XX  
PP 28-FEB-2002.  
XX  
PP 24-AUG-2001; 2001WO-US26550.  
XX  
PP 25-AUG-2000; 2000US-227974P.  
XX  
PA (BADI ) BASF PLANT SCI GMBH.  
XX  
PI Da Costa Silva EO, Ishitani M;  
XX  
DR WPI; 2002-292058/33.  
XX  
PT New Na<sup>+</sup>/H<sup>+</sup> antiporter nucleic acids and proteins, useful e.g. for  
PT modulating stress tolerance in plants, or for detecting, preventing,  
PT conferring resistance to or treating hyperproliferative diseases, e.g.  
PT cankers, galls or tumours -  
XX  
PS Claim 1; Fig 2; 204pp; English.  
XX  
CC The invention relates to novel isolated Na<sup>+</sup>/H<sup>+</sup> antiporter coding nucleic  
CC acid (I) and polypeptides (II). (I) and (II) are useful in modulating the  
CC stress tolerance in a plant, preferably modulating a plant's tolerance  
CC to limited or inadequate water availability, excess salt or osmotic  
CC conditions, excess temperature conditions, excess metal concentration  
CC in soil or water, chemical stress and oxidative stress. These may also  
CC be used as carbon, nitrogen or carbohydrate source, in modulating plant  
CC defence activity, signal transduction, or metabolite transport; or as  
CC probes for the identification and isolation of full length cDNAs or  
CC genomic DNA. The polynucleotides or polypeptides are further used to  
CC detect, prevent, confer resistance to and/or treat hyperproliferative  
CC diseases such as cankers, galls, tumours, and appressorium, increase  
CC plant defence mechanisms against environmental or pathogenic stresses  
CC (e.g. viral, fungal, mycoplasma, bacterial, nematode, herbicidal,  
CC insecticidal, acid rain, drought, or chemical), and hormone synthesis.  
CC The Na<sup>+</sup>/H<sup>+</sup> antiporter coding nucleic acids can be used in creating  
CC transgenic plants with desirable traits, including enhanced plant  
CC defence, drought tolerance, salt tolerance, ultraviolet tolerance,  
CC enhanced flower development and terpene synthesis, in expressing  
CC recombinant proteins to raise antibodies against polypeptides, as  
CC markers for tissues in which the corresponding protein is expressed, as  
CC chromosome markers or tags for chromosome mapping, and for genetic  
CC fingerprinting. The polypeptides are useful in the identification,  
CC prevention, and/or conferment of resistance to plant diseases,  
CC particularly those associated with modulating environmental stress  
CC responses, such as drought, freezing and salt tolerance. The polypeptides  
CC are further useful in modulating plant yield, development,  
CC differentiation, root growth, root morphology, plant colour, plant aroma,  
CC plant flavour, palatability of plant tissue, plant organoleptic  
CC properties, ability to serve as plant nutraceutical, pharmaceutical or  
CC phytochemicals, ability to produce nutraceutical, pharmaceuticals or  
CC phytochemicals of either endogenous or exogenous origin. Antibodies may  
CC be used in diagnostic assays to detect the presence or quantity of the

CC polypeptides, in affinity purification of the polypeptides from  
CC recombinant cell culture or natural sources, and for inhibiting allergic  
CC reactions in animals. The present sequence encodes Physcomitrella patens  
CC Na<sup>+</sup>/H<sup>+</sup> antiporter PpNHX1.  
XX  
SQ Sequence 1674 BP; 426 A; 350 C; 361 G; 537 T; 0 other;  
Query Match 20.7%; Score 482.8; DB 24; Length 1674;  
Best Local Similarity 62.9%; Pred. No. 7.8e-123;  
Matches 801; Conservative 0; Mismatches 462; Indels 11; Gaps 3;  
QY 360 GTGTGTCATCAACCTGTTTCGTCGCGCTGCTCGCGCTGCATCGTCTCGGCCACCTC 419  
DB 79 GTAATTTCAATCTCTCTTTGTTATTTTACTCTGTGCTGCTGCTGCGGCACCTT 138  
QY 420 CTCGAGGAGATCGCTGGTCAATGAGTCCATCACCGGCTCATCATCGGCTCTGCACC 479  
DB 139 CTGGAGGAAATCGGTGGATGAATGAGTCTATTAATCTCTCTCTCTCTCTTTACT 198  
QY 480 GGCCTGTGATCTTGTCTGATGACCAAGGAGAGCTCGCACTTATTCTTCAGTGA 539  
DB 199 GGATCTATAGTGTGATTTCAAGCAAGGTCAAGTCTCATATTCGGAGTTGATGA 258  
QY 540 GATCTCTTCTCATCTACCTCTCTCCCTCCGATCATCTTCAATGCAAGTCTTTCAGTAA 599  
DB 259 GAGCTTTTCTCATATACCTCTCTCCACCTATAATCTTCAATGCTGGTTCAGGTTAA 318  
QY 600 AAAAGCAATCTTCCGGAATTTTCATGAGTACATATTTGGAGCGCTCGGACAAATG 659  
DB 319 AAGAGGAAATCTTTTCGGAATTTTCATAACCAATCATGTTTTTGGAGTTATAGGAGTCTTT 378  
QY 660 ATATCTCTTTTCAATATATCTATTGCTGCCATTTGCAATATTTCAGCAGAAATGAACATTGGA 719  
DB 379 ATTCTTTTCGGAATTTCTCAACAGGAGTTGGTATTCTTCTTCAAGTTCGGACTTAAG 438  
QY 720 ACGTGTGATGTAGAGAAATTTTTCGCAATTGGAGCAATCTTTTCTCGGACAGATTCGTGTC 779  
DB 439 AACCTGCTATTTCAGATATCTTAGCTATTGGAGTCACTCTTTCTGTACCGATTCCGTC 498  
QY 780 TGACATTTGAGGTCCTCAATCAGGATGAGACACCCCTTTTGTACAGTCTGGTATTCGGT 839  
DB 499 TGACATTTGAGGTCCTCAACAGGAGTTGGTATTCTTCTTCAAGTTCGGACTTAAG 558  
QY 840 GAAGGTGTTGTAACGATGCTATCAATTAATGTTCTTCAACGCACTACAGAACTTTGAT 899  
DB 559 GAAGGATGCTTAATGATGCTACTTCTGTGTTCTGTCTCGAGCTGTTCAACATACAAC 618  
QY 900 CTGTTCACATAGATGCGGCTGCTGTTCTGAAATTTCTTGGGGAACCTCTTTTATTTATTT 959  
DB 619 TTTGACAAATTTTACATCTTTAGAGGCTTACAAATTTGGAGGCACTTTCTTGTACTTATTC 678  
QY 960 TTGTGAGACACCTTCTTGGAGTATTGCTGGATTGCTCAGTGCATACATATCAAGAA 1019  
DB 679 TTCTCGAGTTGCAATCTTGGGAATGCGCTCGGCTTAAATAGCGCATATATATCAAGACA 738  
QY 1020 CTATACATTTGAAAGGCAATCTTACTGACCGTGAGGTTGCCCTTATGATGCTCATGGCTTAC 1079  
DB 739 ATGTACTTTGCGAGGCAATCCACGGATCGTGAATAGCAATCATGACATTCATGCGGTAT 798  
QY 1080 CTTTCATATAGCTGGCTGAGTGTAGATTGAGCGGCAATCTTCACGGTATTTCTTCTGT 1139  
DB 799 TTATCTTACGCTCTTTCAGAGGCTTTTCTACTTGTAGTGAATTTCTCTCAGTGTCTTTTGC 858  
QY 1140 GGTATTGTTAATGTACATTTACATTTGSCATAAGCTACAGAGAGTTTCAAGAGTTTACAACA 1199  
DB 859 GGCATTTGTAATGTCTCATTTACATTTGGCAATAGCTCAGGAGAAATTCGAATCACAAGC 918  
QY 1200 AAGCAGCATTTGCAATCTGTCTCTTCAATGCTGAGACTTTTCTTCTCTGTATGTTGGG 1259  
DB 919 AAGCATTTCTTTGCAAGGATGTCAATTCATTCGAGAGAGGTTTCATATTTCTATATGTTGA 978  
QY 1260 ATGATGTCATTTGATATTTGAAATTTGGAGTTGCGGAGTTCAGACCTCGCAATTCATTT 1319







XX AAC95372;  
 AC 19-FEB-2001 (first entry)  
 DT  
 DE Cat flea HMT Na/H transporter cDNA ORF, SEQ ID NO:1870.  
 XX  
 XX Cat flea; hindgut and Malpighian tubule nucleic acid; HMT;  
 XX flea infestation; vaccine; antiparasitic; therapeutic target;  
 KW diagnosis; detection; ss.  
 KW  
 XX Ctenocephalides felis.  
 XX WO200061621-A2.  
 XX  
 XX 19-OCT-2000.  
 XX  
 XX 07-APR-2000; 2000WO-US09437.  
 PF  
 XX 09-APR-1999; 99US-0128704.  
 XX  
 XX (HESK-) HESKA CORP.  
 XX  
 XX Brandt KS, Gaines PJ, Stinchcomb DT, Wisniewski N;  
 PI WPI; 2000-656323/63.  
 XX P-PSDB; AAB29621.  
 DR  
 DR  
 XX  
 XX Flea Malpighian tubule and head and nerve cord tissue derived nucleic  
 PT acids useful for the prevention, diagnosis and treatment of flea  
 PT infestations -  
 XX  
 XX Claim 1; Page 894-895; 964pp; English.  
 XX  
 CC The invention relates to novel cat flea (*Ctenocephalides felis*) nucleic  
 CC acids which are expressed in hindgut and Malpighian tubule (HMT) tissue  
 CC or head and nerve cord (HNC) tissue. The invention also relates to the  
 CC encoded proteins. The invention additionally encompasses expression  
 CC constructs, recombinant viruses and recombinant cells comprising the  
 CC nucleic acids of the invention, recombinant production of the proteins,  
 CC antibodies against the proteins, a method of identifying inhibitors of  
 CC the proteins, and compositions comprising the inhibitors for  
 CC administration to an animal. The nucleic acids, and the proteins they  
 CC encode may be used in the prevention, treatment and diagnosis of diseases  
 CC associated with flea infestations. For example, the nucleic acids may be  
 CC used to produce an HMT or HNC protein according to standard recombinant  
 CC DNA methodology by inserting the nucleic acids into a host cell and  
 CC culturing the cell to express the protein. The HMT and HNC nucleic acids  
 CC may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect  
 CC and quantitate the presence of cat flea or other homologous nucleic acid  
 CC sequences in samples. They may also be used to study the expression and  
 CC function of the proteins and their role in metabolism. The HMT and HNC  
 CC proteins may be used as antigens in the production of specific  
 CC antibodies, and in assays to identify modulators (agonists and  
 CC antagonists) of HMT and/or HNC protein expression and activity. The  
 CC anti-HMT/HNC protein antibodies and antagonists may also be used to  
 CC downregulate protein expression and activity. The antibodies may also be  
 CC used as diagnostic agents for detecting the presence of flea polypeptides  
 CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The  
 CC present sequence represents a cat flea HMT cDNA of the invention.  
 XX  
 XX Sequence 1824 BP; 529 A; 330 C; 355 G; 610 T; 0 other;  
 SQ  
 Query Match 4.7%; Score 109.4; DB 21; Length 1824;  
 Best Local Similarity 47.8%; Pred. No. 1.9e-19;  
 Matches 351; Conservative 0; Mismatches 381; Indels 3; Gaps 1;  
 KY 546 TTCTTTCATCTACCTCCCTCCCGATCATCTTCAATGAGGTTTTCAGGTAAAGAAAAG 605  
 Db 445 TTTTCTTAGTGCTTCTACCGCTATATATTGAAATCCGGGTATATTTTCATAAAGGT 504  
 KY 606 CAAATCTTCGGGATTTTCATGCGATGCACATTTATTTGAGCGCTCGGACATATATCC 665  
 Db 505 AATTTTTTCAAAATATTTGGTTCCATCTCGTGTGTTGCTATATTTTGAACAGCCATATCA 564  
 KY 666 TTTTTCACATATCTATTTGCTGCCATTCGAATATTTCAGCAGAAATGAACATTTGGAAACGCTG 725  
 Db 565 GCCTTTGTTGTCGGTGTGTTGTTTACTAGGAATGGCAGATGTTGCTTATAACTTA 624  
 KY 726 GATGTAGAGATTTTCTTGAATTTGGAGCCATCTTTCTGCGACAGATCTCTGCTGACACA 785  
 Db 625 AGCTTTGTTGAATCCTTTGCTTTTCCGTTTCATTAATTTCTGCAAGTAGCCCTGTAGTACC 684  
 KY 786 TTGAGGTCCTCAA--TCAGGATGAGACACCTTTTGTGTACAGTCTGTTGATTCGGTGAA 842  
 Db 685 GTAGCTATTTTCCATGCTTTAGACGTGGACCCAGTTTAAACATGTTGGTTCGGAGAA 744  
 KY 843 GGTGTTGGAACGATGCTACATCAATTTGTGCTTTTAAACGCACTACAGAACTTTGATCTT 902  
 Db 745 AGTATTTTAAATGATGCTATTTTCAATTTGTTTAAACAGTGCAGTTTGGAAATCCAACAT 804  
 KY 903 GTCCACATAGATGCGGCTGCTGTTCTGAAATTTCTTGGGAACTTCTTTTATTTATTTTGG 962  
 Db 805 CCTTTAATGACGACTGCTGTAAGCTGTAGTCTCCGTTTAAATAGGTTTGTGTTTATGTTTC 864  
 KY 963 TCGAGCACCTTCTTGGAGTATTTGCTGGAATGCTCAGTGCATACATAATCAAGAAAGCTA 1022  
 Db 865 TTTGCTTCGGCTGTATCGGTGTAGTCTTTGCTTAATTTAGTGTCTTTTGTGAAACAT 924  
 KY 1023 TACATTTGGAAGCAATTTACTACCGTGCAGGTGCGCTTATGATGCTCATGCTTACCTT 1082  
 Db 925 GTTGATCTTGAAGAATATCCGTTTACGTTAGGTTAGTATGATGTTGGTGTACTTATGCA 984  
 KY 1083 TCATATATGCTGGCTGAGTTGCTAGATTTAGCGGCATTTCTACCGTATTTCTTCTGTTGGT 1142  
 Db 985 CCTTATGTTTGGCAGAGAGAAATTCATTTATCAGGTATTAATGGCGATATTTCTGTGCGC 1044  
 KY 1143 ATTGTAATGTCACATTACACTTTGGCATAAACGTCACAGAGAGTTCAAGAGTTACACAAAG 1202  
 Db 1045 ATTTGATGTCCTTACATACACATTTCAATTTATCAACGGTTACACAAATAACTATGCGAG 1104  
 KY 1203 CACGCAATTTGCAACTCTGCTCTTCAATCTGAGACTTTTCTCTCTGTATGTTGGGATG 1262  
 Db 1105 CAGACGATGAGAACTTGGCTTTTATTCAGAAACTTGTGTGTTGTTGTTTATTTAGGAATG 1164  
 KY 1263 GATGCAATTTGATATT 1277  
 Db 1165 GCTATATTTAGTTTT 1179  
 RESULT 15  
 AAC95373/c  
 ID AAC95373 standard; cDNA; 1824 BP.  
 XX  
 AC AAC95373;  
 XX  
 DT 19-FEB-2001 (first entry)  
 XX  
 DE Cat flea HMT Na/H transporter cDNA ORF complement, SEQ ID NO:1871.  
 KW Cat flea; hindgut and Malpighian tubule nucleic acid; HMT;  
 KW flea infestation; vaccine; antiparasitic; therapeutic target;  
 KW diagnosis; detection; ss.  
 XX  
 OS Ctenocephalides felis.  
 XX  
 PN WO200061621-A2.  
 XX  
 PD 19-OCT-2000.  
 XX  
 PF 07-APR-2000; 2000WO-US09437.  
 XX  
 PR 09-APR-1999; 99US-0128704.  
 XX  
 XX (HESK-) HESKA CORP.  
 PA  
 XX

PI Brandt KS, Gaines PU, Stinchcomb DT, Wisniewski N;

XX WPI; 2000-656323/63.

DR P-PSDB; AAB29621.

XX Flea Malpighian tubule and head and nerve cord tissue derived nucleic acids useful for the prevention, diagnosis and treatment of flea infestations -

XX Claim 1; Page 895-896; 964pp; English.

XX The invention relates to novel cat flea (*Ctenocephalides felis*) nucleic acids which are expressed in hindgut and Malpighian tubule (HMT) tissue of head and nerve cord (HNC) tissue. The invention also relates to the encoded proteins. The invention additionally encompasses expression constructs, recombinant viruses and recombinant cells comprising the nucleic acids of the invention, recombinant production of the proteins, antibodies against the proteins, a method of identifying inhibitors of the proteins, and compositions comprising the inhibitors for administration to an animal. The nucleic acids, and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with flea infestations. For example, the nucleic acids may be used to produce an HMT or HNC protein according to standard recombinant DNA methodology by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The HMT and HNC nucleic acids may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect and quantitate the presence of cat flea or other homologous nucleic acid sequences in samples. They may also be used to study the expression and function of the proteins and their role in metabolism. The HMT and HNC proteins may be used as antigens in the production of specific antibodies, and in assays to identify modulators (agonists and antagonists) of HMT and/or HNC protein expression and activity. The anti-HMT/HNC protein antibodies and antagonists may also be used to downregulate protein expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of flea polypeptides in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The present sequence represents a cat flea HMT cDNA of the invention.

XX Sequence 1824 BP; 610 A; 355 C; 330 G; 529 T; 0 other;

Query Match 4.7%; Score 109.4; DB 21; Length 1824;

Best Local Similarity 47.8%; Pred. No. 1.9e-19;

Matches 351; Conservative 0; Mismatches 381; Indels 3; Gaps 1;

Qy 546 TTCTTCATCTACCTCCCTCCGATCATCTTCAATGAGGTTTTCAGGTAAAGAAAAG 605

Db 1380 TTTTCTTAGTGCTTCTACCGCTATAATTTGAATCCGGGTATAATTTGCATAAAGGT 1321

Qy 606 CAATTTCTCCGGAATTCATGAGCATACATATTATTTGGAGCCGTCGGACATGATATCC 665

Db 1320 AATTTTTTCAAAATATGGTTTCCATCTCGGTGTGCTATATTGGAAACACCATATCA 1261

Qy 666 TTTTTCACATATCTATTGTGCCATTGCAATATTTCAGCAGATGAACATTTGGAAACGCTG 725

Db 1260 GCCTTTGTGTGCGTGCTGGTGTGTTACTAGGAATGGCAGATGTGCTTATAACTTA 1201

Qy 726 GATGTAGAGATTTTTCGCAATTGGAGCCATCTTTCTCGCAGACAGATTCGTCTGCACA 785

Db 1200 AGCTTTGTGTAATCCTTTGCTTCCGTTTCATTAATTTCTGCAGTAGACCCCTGTAGTACC 1141

Qy 786 TTGCAGGTCTCTCAA---TCAGGATGAGACACCCCTTTTGTACAGTCTGGTATTCGGTGA 842

Db 1140 GTAGCTATTTCCATGCTTTAGAGCTGGAGCCAGTTTTTAAACATGTGTTGTTTCGGAGAA 1081

Qy 843 GGTGTGTGAACGATGCTACATCAATTGTGCTTTTCAACGCACTACAGAACTTTTGATCTT 902

Db 1080 AGTATTTTAAATGATGCTATTTTCAATTTGTTTAAACAACCTGCAGTTTGGATCCACAAT 1021

Qy 903 GTCCACATAGATCGGCTGTCTGTAATTTCTGGGAACTTCTTTTATTTATTTTGG 962

Db 1020 CCTTTAATGACGACTGTGAAGCTGTAGTCTCCGGTTTAAATAGGTTTGTGTTAATGTTTC 961

Qy 963 TCGAGCACCTTCCCTTGGAGTATTTTGTGGAATTTGCTCAGTGCATACATAATCAAGAAGCTA 1022

Db 960 TTTGCTTCGGCTGGTATCGGTAGTCTTTGCCCTTAATTAGTGTCTTTTGTGTTGAAACAT 901

Qy 1023 TACATTGGAAGGCATTCTACTGACCGGTGAGGTTGCCCTTATGATGCTCATGGCTTACCTT 1082

Db 900 GTTGATCTTTAGAAAGTATCCGCTCCTTAGAGTTAGGTATGATGTTGGTGTGTTACTTATGCA 841

Qy 1083 TCATATATGCTGGCTGAGTTGCTAGATTTGAGCGCATTTCCACCGTATTTCTTCTGTGGT 1142

Db 840 CCTTAATGTTTGGCAGAAGGAATTCATTATCAGGTATAATGGCGATATATTCTGTGGC 781

Qy 1143 ATTGTAATGTCAATTTACACTTTGGCATAACTTCACAGAGGTTCAAGAGTTACAAACAAG 1202

Db 780 ATTGTGATGTCCCATTTACACACATTTCAATTTATCAACGGTTACACAATAACTATGCA 721

Qy 1203 CACGATTTGCAACTCTCTCTTCAATTCCTGAGACTTTTCTCTTCTGATGTTGGGATG 1262

Db 720 CAGACGATGAGAATCTTGGCTTTTATTGCAGAACTTGTGTGTTGCTTATTTAGGAATG 661

Qy 1263 GATGCATTGGATATT 1277

Db 660 GCTATATTAGTTTT 646

Search completed: April 5, 2003, 12:58:35

Job time : 549 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 12:44:33 ; Search time 92 Seconds  
(without alignments)  
7766.922 Million cell updates/sec

Title: US-09-888-035A-1  
Perfect score: 2330  
Sequence: 1 gagaagagagatttttagcg.....ttgaaaaaaaaaaaaaaaaa 2330

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: \*  
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2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62.6	2.7	2574	2	US-08-677-734A-8
2	62.6	2.7	2574	4	US-09-097-053-8
C 3	44.6	1.9	3489	2	US-08-728-323A-1
C 4	44.6	1.9	3489	4	US-09-298-568-1
5	44.6	1.9	32207	2	US-08-770-379-20
6	44.6	1.9	32207	4	US-08-757-669A-20
7	44.6	1.9	32207	4	US-09-230-371A-20
8	42.8	1.8	1100	4	US-09-372-422A-47
9	42.4	1.8	7218	1	US-08-232-463-14
10	42.4	1.8	68750	3	US-09-335-409-1
11	42.4	1.8	68750	4	US-09-568-102-1
12	42.4	1.8	68750	4	US-09-567-969-1
13	42.4	1.8	68750	4	US-09-568-480-1
14	42.4	1.8	68750	4	US-09-568-486-1
15	42.4	1.8	68750	4	US-09-568-472-1
16	42.4	1.8	68750	4	US-09-567-899-1
17	40.4	1.7	1525	6	5229279-1
18	40	1.7	2064	1	US-08-343-428-1
19	39.6	1.7	7218	1	US-08-232-463-14
C 20	39.4	1.7	1355	3	US-08-415-655-14
21	38.8	1.7	1524	6	5512669-1
C 22	38.8	1.7	1833	2	US-08-403-852D-6
23	38.8	1.7	1833	3	US-08-510-646B-6
24	38.8	1.7	1833	4	US-09-231-818-6
C 25	38.6	1.7	795	2	US-08-997-080-46
C 26	38.6	1.7	795	2	US-08-997-362-46
C 27	38.6	1.7	795	3	US-08-873-970-46

Sequence 46, Appl  
Sequence 46, Appl  
Sequence 46, Appl  
Sequence 46, Appl  
Sequence 46, Appl  
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Sequence 12, Appl  
Sequence 12, Appl  
Sequence 15, Appl  
Sequence 12, Appl  
Sequence 12, Appl  
Patent No. 5248670  
Sequence 3, Appl  
Sequence 3, Appl  
Sequence 3, Appl  
Sequence 2, Appl  
Sequence 2, Appl

Sequence 46, Appl  
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Sequence 46, Appl  
Sequence 46, Appl  
Sequence 46, Appl  
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Sequence 15, Appl  
Sequence 12, Appl  
Sequence 12, Appl  
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Sequence 2, Appl  
Sequence 2, Appl

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Sequence 46, Appl  
Sequence 46, Appl  
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Sequence 12, Appl  
Sequence 12, Appl  
Sequence 15, Appl  
Sequence 12, Appl  
Sequence 12, Appl  
Patent No. 5248670  
Sequence 3, Appl  
Sequence 3, Appl  
Sequence 3, Appl  
Sequence 2, Appl  
Sequence 2, Appl

#### ALIGNMENTS

#### RESULT 1

US-08-677-734A-8  
; Sequence 8, Application US/08677734A  
; Patent No. 5871919  
; GENERAL INFORMATION:  
; APPLICANT: Brant, Steven R.  
; APPLICANT: Yun, Chris C.H.  
; APPLICANT: Donowitz, Mark  
; APPLICANT: Tse, Chung-Ming  
; TITLE OF INVENTION: Cloning, Tissue Distribution, and  
; TITLE OF INVENTION: Functional Analysis Of The Human Na+/H+ Exchanger Isoform,  
; TITLE OF INVENTION: NHE3.  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESS: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/677,734A  
; FILING DATE: 10-JUL-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fordis, Jean B.  
; REGISTRATION NUMBER: 32,984  
; REFERENCE/DOCKET NUMBER: 05387.0043-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 408-4000  
; TELEFAX: (202) 408-4400  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2574 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-677-734A-8

Query Match 2.7%; Score 62.6; DB 2; Length 2574;

Best Local Similarity 44.8%; Pred. No. 9e-08; Mismatches 399; Indels 9; Gaps 2;  
Matches 331; Conservative 0;

544	QY	TC	TCTCTCATCTAC	CTCCTCCCTCCGATCATCTTCAATG	CAGGTTTTCAGGTAAGAAA	603	
341	DB	TC	TCTCTCTTCTAC	TGCTGCTGCCCCATCGTGTGGA	CGCGGCTACTTCATGCCCAC	400	
604	QY	AG	CAATTCCTTCG	GAATTCATGACATCACATATTTTGG	AGCGCTCGGCAATGATAT	663	
401	DB	GC	CTCTCTTC	TGCGAACCTG	GGGACCATCTGTGTACGCGCTGTGGGTACCGTGTGGA	460	
664	QY	CT	TTTTTCA	CAATATCTATTGCTGCCAATGCAATATTCAG	CAGAAATGAACATGGAACGC	723	
461	DB	AC	GCGGCAC	CAACCGGGCTGCTCCCTCTACGCGCTCTTCT	CAGTGGGCTCATGCGGCACC	520	
724	QY	TG	GATGTAG	A-----GATTTTCTTGCAATTTGGAGCCATCTTT	TCGCGACAGATCTG	777	
521	DB	TG	CAGATTGGCG	TGCTGGGACTTCTCCTGTTTGGCAGCTCAT	TGGCGCTGTGGACCCGG	580	
778	QY	TC	TGC	CATATG	CAGTCCCATCAGG---ATGAGACACCCCTTTTGTG	834	
581	DB	TG	CGCGTCT	TGGCGGTGTGTGAGGAGTCCATGTCAAC	AGAGTCTGTTTCATCATCTGCT	640	
835	QY	TC	GGTGA	AGGTGTGTGAACGATGCTACATCAATTTGTGCTTTT	CAACGCACTACAGAACT	894	
641	DB	TC	GGGAGT	CGTCTGAACGACGAGTCACCGTGGTCTGTCA	ATGTGTTTGAATCTT	700	
895	QY	TT	GA	CTTTG	CCATATAGATGCGGCTGTCGTTCTGAAATCTTTGGG	954	
701	DB	TC	GTGGCGCT	TGGGAGGTGCAACGCTGACTGGCGTGGACTGCGT	GAAAGGCGATAGTGCTCT	760	
955	QY	TA	TTTTTGT	CGACACCTTCTCTGGAGTATTTGCTGGATTTGCT	CAGTGCATACATATCA	1014	
761	DB	TC	TTCTG	TG	TGAGCCTTGGGGGCA	CGCTGGTGGGGTGGTCTTCTG	820
1015	QY	AGA	AGCTATACAT	TGGAAGCCATTCTACTGACCGT	GAGTTGGCCTTATGATGCTCATGG	1074	
821	DB	TG	GTAG	CGCGCTTACCACGATATGCGGTATCAT	CGCCCGGCTTCGTGTTCATCATCT	880	
1075	QY	CT	TACCTTT	CATATATGCTGGCTGAGTTGCTAGATTTT	GAGCGGCATTTCTACCGCTATTCT	1134	
881	DB	CCT	ACCTGTCT	ACCTGACGTC	CGAGATGCTGTGCGCCATCTCGCCATCACCT	940	
1135	QY	TC	TGTGGTAT	TGTAATGTACATATACATTTG	CGCATAAAGTACAGAGTTCAAGAGTTA	1194	
941	DB	TC	TGTGG	CAATCTGCTCAGAAAGTATGTGAAG	GGCCAAACATCTCGAGCAGTCGCGCCACCA	1000	
1195	QY	CA	ACAAAG	CAGCATTTGCAACTCTGTCTCTTCA	TTTGTGAGACTTTTCTCTTCTCTGTATG	1254	
1001	DB	CC	GTGG	CTACACCATGAAGATGCTGGCCAG	CGCGCGAGACCATCATCTTCA	1060	
1255	QY	TT	GGGAT	TGGATGCA	TTTGGGA	1273	
1061	DB	TG	GGTATCT	CGGCGGTGA	1079		

## RESULT 2

US-097-053-8  
Sequence 8, Application US/09097053  
Patent No. 6392025  
GENERAL INFORMATION:  
APPLICANT: Brant, Steven R.  
APPLICANT: Yun, Chris C.H.  
APPLICANT: Donowitz, Mark  
APPLICANT: Tse, Chung-Ming  
TITLE OF INVENTION: Cloning, Tissue Distribution, and  
Functional Analysis Of The Human Na+/H+ Exchanger Isoform,  
NHE3.  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA







[illegible]

```

RESULT 8
US-09-372-422A-47
; Sequence 47, Application US/09372422A
; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Barrieu
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 1100
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (94) ... (835)
US-09-372-422A-47

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	Query Match	1.8%;	Score 42.8;	DB 4;	Length 1100;
	Best Local Similarity	51.6%;	Pred. No. 0.027;		
	Matches 98;	Conservative	0;	Mismatches 92;	Indels 0; Gaps 0;
QY	297	ATGGGGATGGAGTGGCGGCGCGCGGTGGGGGCTCTGTACACACCTCCGACTACGCG	356		
Db	520	ATGGAGATCGTATCATCCTTCGCGCTGTTGTACACCGTGTACGCCACCGCGCGCACCG	579		
QY	357	TCGCTGTGTGCCATCAACCTGTTTCGTGCGGTGCTCTGCGGCTCGATGTCCTCGGCGAC	416		
Db	580	AAGAAAGGGGTCCCTGGGCACCATCGCGGCCATGCGCCATCGGCTTCATCGTCGGCGCCAAAC	639		
QY	417	CTCCTCGAGGAGATCGCTGGGTCNAATAGTTCATACCGCGCTCATCATCGGCTCTGC	476		
Db	640	ATCTGGCGCGCGGCGCCCTTCAGCGGCGGCTCCATGAACCCGGCGGCTCCTTCGGGCCCC	699		
QY	477	ACGGCGCTGG	486		
Db	700	GCCTGGCGG	709		

```

RESULT 9
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
;

```

COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZgpt-F15  
US-08-232-463-14

[illegible]

RESULT 10  
 US-09-335-409-1  
 ; Sequence 1, Application US/09335409  
 ; Patent No. 6121029  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schupp, Thomas  
 ; APPLICANT: Ligon, James  
 ; APPLICANT: Molnar, Istvan  
 ; APPLICANT: Zirkle, Ross  
 ; APPLICANT: Cyr, Devon  
 ; APPLICANT: Goerlach, Joern  
 ; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES  
 ; FILE REFERENCE: 4-30582A  
 ; CURRENT APPLICATION NUMBER: US/09/335,409



Query Match 1.8%; Score 42.4; DB 4; Length 68750;  
Best Local Similarity 49.5%; Pred. No. 0.44;  
Matches 109; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 311 GCGCGCGCGCGCTGGGGCTCTGTACACGACCTCCGACTACGCGTGGTGTCTCCAT 370  
DB 4350 GCGCGCGTGGGGACGCTGCGCTTGTCTGGCGACCGACGCGCGGAAGTCTGCC 4409

QY 371 CAACCTGTTCTGCGCTGCTCTGCGCTGCATCTCTCGGCCACCTCTCCGAGGAGAA 430  
DB 4410 CGCGCGCTCGCGCGCGCTCGCGGGCTCAGGGGACGAGCGCGCTCTGGCGGT 4469

QY 431 TCGCTGGTCAATGAGTCCATCACCGCGCTCATCGGGCTTCGACCGCGCTCTCCGAGGAGAA 430  
DB 4470 GGGCTGAACATGAAGGCGCGCGACCTCATCTCGCATCTCGCGCTCGAGCTCGG 4529

QY 491 CTTCGTGATGACCAAGGAAGAGCTCGCACTTATTTCGTC 530  
DB 4530 GCTCTCTCCACGAGGCTTATACGATGTACGCGCTCGTC 4569

RESULT 14  
US-09-568-486-1  
; Sequence 1, Application US/09568486  
; Patent No. 635459  
; GENERAL INFORMATION:  
; APPLICANT: Schupp, Thomas  
; APPLICANT: Ligon, James  
; APPLICANT: Molnar, Istvan  
; APPLICANT: Zirkle, Ross  
; APPLICANT: Cyr, Devon  
; APPLICANT: Goerlach, Joern  
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES  
; FILE REFERENCE: 4-30582A  
; CURRENT APPLICATION NUMBER: US/09/568,486  
; PRIOR FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: 09/335,409  
; PRIOR FILING DATE: 1999-06-17  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 68750  
; TYPE: DNA  
; ORGANISM: Sorangium cellulosum  
US-09-568-486-1

Query Match 1.8%; Score 42.4; DB 4; Length 68750;  
Best Local Similarity 49.5%; Pred. No. 0.44;  
Matches 109; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 311 GCGCGCGCGCGCTGGGGCTCTGTACACGACCTCCGACTACGCGTGGTGTCTCCAT 370  
DB 4350 GCGCGCGTGGGGACGCTGCGCTTGTCTGGCGACCGACGCGCGGAAGTCTGCC 4409

QY 371 CAACCTGTTCTGCGCTGCTCTGCGCTGCATCTCTCGGCCACCTCTCCGAGGAGAA 430  
DB 4410 CGCGCGCTCGCGCGCGCTCGCGGGCTCAGGGGACGAGCGCGCTCTGGCGGT 4469

QY 431 TCGCTGGTCAATGAGTCCATCACCGCGCTCATCGGGCTTCGACCGCGCTCTCCGAGGAGAA 430  
DB 4470 GGGCTGAACATGAAGGCGCGCGACCTCATCTCGCATCTCGCGCTCGAGCTCGG 4529

QY 491 CTTCGTGATGACCAAGGAAGAGCTCGCACTTATTTCGTC 530  
DB 4530 GCTCTCTCCACGAGGCTTATACGATGTACGCGCTCGTC 4569

RESULT 15  
US-09-568-472-1  
; Sequence 1, Application US/09568472  
; Patent No. 6358719  
; GENERAL INFORMATION:

; APPLICANT: Schupp, Thomas  
; APPLICANT: Ligon, James  
; APPLICANT: Molnar, Istvan  
; APPLICANT: Zirkle, Ross  
; APPLICANT: Cyr, Devon  
; APPLICANT: Goerlach, Joern  
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES  
; FILE REFERENCE: 4-30582A  
; CURRENT APPLICATION NUMBER: US/09/568,472  
; CURRENT FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: 09/335,409  
; PRIOR FILING DATE: 1999-06-17  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 68750  
; TYPE: DNA  
; ORGANISM: Sorangium cellulosum  
US-09-568-472-1

Query Match 1.8%; Score 42.4; DB 4; Length 68750;  
Best Local Similarity 49.5%; Pred. No. 0.44;  
Matches 109; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 311 GCGCGCGCGCGCTGGGGCTCTGTACACGACCTCCGACTACGCGTGGTGTCTCCAT 370  
DB 4350 GCGCGCGTGGGGACGCTGCGCTTGTCTGGCGACCGACGCGCGGAAGTCTGCC 4409

QY 371 CAACCTGTTCTGCGCTGCTCTGCGCGCTGCATCTCTCGGCCACCTCTCCGAGGAGAA 430  
DB 4410 CGCGCGCTCGCGCGCGCTCGCGGGCTCAGGGGACGAGCGCGCTCTGGCGGT 4469

QY 431 TCGCTGGTCAATGAGTCCATCACCGCGCTCATCGGGCTTCGACCGCGCTCTCCGAGGAGAA 430  
DB 4470 GGGCTGAACATGAAGGCGCGCGACCTCATCTCGCATCTCGCGCTCGAGCTCGG 4529

QY 491 CTTCGTGATGACCAAGGAAGAGCTCGCACTTATTTCGTC 530  
DB 4530 GCTCTCTCCACGAGGCTTATACGATGTACGCGCTCGTC 4569

Search completed: April 5, 2003, 15:59:11  
Job time : 288 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 14:52:33 ; Search time 210 Seconds  
(without alignments)  
9732.385 Million cell updates/sec

Title: US-09-888-035A-1

Perfect score: 2330

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*

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- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq\*
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- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	768.8	33.0	1617	9	US-09-938-842A-1239
2	766.8	32.9	2136	9	US-10-155-535-1
3	711	30.5	2066	9	US-10-155-535-3
4	138.8	6.0	281	10	US-09-294-0938-2697
5	77	3.3	1800	9	US-10-155-535-5
6	66.8	2.9	1688	10	US-09-800-729-57
7	65	2.8	1581	10	US-09-800-729-22
8	58.4	2.5	4598	9	US-09-822-846-118
9	52.4	2.2	1354	10	US-09-800-729-58
10	51.4	2.2	1935	9	US-10-217-096-3
11	51.4	2.2	3537	9	US-10-217-096-1
12	44.4	1.9	1305	10	US-09-815-242-7730
13	43.4	1.9	1883	12	US-10-033-109-9
14	43	1.8	690	10	US-09-887-576-816
15	42.6	1.8	325	9	US-10-040-739-929
16	42.6	1.8	88421	9	US-09-976-059-1
17	42.4	1.8	68750	9	US-10-014-717-1
18	41.2	1.8	1827	10	US-09-887-576-817
19	41	1.8	520	9	US-10-184-644-332

20	40.4	1.7	984	10	US-09-815-242-7872	Sequence 7872, Ap
c 21	40	1.7	916	9	US-10-184-644-78	Sequence 78, Appl
c 22	40	1.7	22960	10	US-09-070-927A-345	Sequence 345, Appl
23	39.8	1.7	2248	9	US-10-125-237-11	Sequence 11, Appl
24	39.6	1.7	1413	10	US-09-805-467A-1	Sequence 1, Appl
25	39.6	1.7	1461	9	US-10-006-950-1	Sequence 1, Appl
26	39.6	1.7	2300	10	US-09-805-467A-3	Sequence 3, Appl
c 27	39.4	1.7	747	10	US-09-887-576-781	Sequence 781, Appl
c 28	39.4	1.7	774	10	US-09-770-445-902	Sequence 902, Appl
29	39.4	1.7	1428	12	US-10-023-673-3	Sequence 3, Appl
30	39.4	1.7	2150	12	US-10-044-090-675	Sequence 675, Appl
31	39.4	1.7	2625	12	US-10-023-673-1	Sequence 1, Appl
c 32	39.2	1.7	1898	10	US-09-768-826-22	Sequence 22, Appl
c 33	38.8	1.7	431	10	US-09-864-761-23962	Sequence 23962, A
c 34	38.8	1.7	573	10	US-09-864-761-7231	Sequence 7231, Ap
35	38.8	1.7	1758	10	US-09-815-242-7825	Sequence 7825, Ap
36	38.8	1.7	1944	10	US-09-864-761-2825	Sequence 2825, Ap
37	38.8	1.7	3826	10	US-09-927-091-3	Sequence 3, Appl
c 38	38.6	1.7	23433	10	US-09-927-091-7	Sequence 7, Appl
c 39	38.6	1.7	795	9	US-10-051-643-46	Sequence 46, Appl
c 40	38.6	1.7	795	9	US-09-880-505-46	Sequence 1, Appl
41	38.6	1.7	2040	10	US-09-733-300-1	Sequence 12, Appl
42	38.6	1.7	2040	10	US-09-733-300-12	Sequence 1, Appl
43	38.6	1.7	2080	9	US-10-003-392-1	Sequence 949, Appl
44	38.4	1.6	5431	10	US-09-834-375-949	Sequence 28059, A
45	38.2	1.6	327	10	US-09-864-761-28059	

#### ALIGNMENTS

#### RESULT 1

US-09-938-842A-1239  
; Sequence 1239, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 1239  
; LENGTH: 1617  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-1239

Query Match 33.0%; Score 768.8; DB 9; Length 1617;

Best Local Similarity 68.6%; Pred. No. 4.7e-230; Indels 6; Gaps 1;  
Matches 1077; Conservative 0; Mismatches 487;

QY	329	GGCTCTGTACACGACCTCCGACTACCGCTCGGTGGTGTCCATCAACCTGTTGTCGCGCT	388
Db	27	GCCTTCGTTATCGACATCTGATCAGCTTCTGTGGTGGTTCGATCTCTTTGTTCACT	86
QY	389	GCTCTCGGCTGATCGTCTCGGCCACCTCTCTCGAGGAGATCGTGGGTCAATGATC	448
Db	87	TCTTTGCTGTATTGTTCTTGGTTCATCTTTTGAAGAGATAGATGATGAACGAATC	146
QY	449	CATCAGCGGCTCATCATCGGCTCTGACCGCGGTGGTGTCTTCTGCTGATCACCAGG	508
Db	147	CATCAGCGGCTTGTGATTGGCTAGGCACCTGGTGTACCATTTTGTGATTAGTAAGG	206





Db 644 ATGCAGGGTTTCAAGTAAAGAGGAGCGATTTTTCGAAATTTTGTAACTATTATGGCTT 703  
Qy 640 TTGAGCGGTGGGACAAATGATATCTTTTTCACAAATATCTATTGCTGCGCAATTCGAATAT 699  
Db 704 TTGCGCAATTGGGACCGTAGTTTCTTGACCAATAATATCTAGGTGCAATTCAGTTCT 763  
Qy 700 TCAGCAGATGAACATTTGGAACGCTGGATGTAGGAGATTTTCTTGCAATTTGGAGCCATCT 759  
Db 764 TTAAGAAATAGACATTTGGGACCTTTGACTTGGCGGATTTTCTTGCAATCGGCGCCATAT 823  
Qy 760 TTTCTGGACAGATCTGTCTGACATTTGAGAGCTTCTCAATCAGATGAGACACCTTTT 819  
Db 824 TTGCTGAACCGACTCTGTATGACACACTACAGAGTTCTCAATCAAGATGAGACACCTTTGC 883  
Qy 820 TGTACAGTCTGGTATTCGGTGAAGCTGTGTGAACGATGCTACATCAATTTGCTTTTCA 879  
Db 884 TTTACAGTCTGTATTTGGAGAGGCGTTGTGAATGATGCCAATCTGTTGTGCTCTTCA 943  
Qy 880 ACGCACTACAGAACTTTGATCTTGTCCACATAGATGGCGCTGTGTTCTCGAAATTTCTGG 939  
Db 944 ATGCTATTACAGATTTTGACCTACCCACCTTAACCATGAAGCAGCTTTTCAATTTCTTG 1003  
Qy 940 GGAACCTCTTTTATTTATTTTTCGAGACCTTCTCTTGAGATTTTGTCTGGATTTGCTCA 999  
Db 1004 GGAACCTTTTATCTGTTTCTCTTGAGCACCGGACTTGGTGTGCAACTGGTCTGATAA 1063  
Qy 1000 GTGCATACATAATCAAGAAGCTATACATTTGGAAGGCACTTCTACTGACCGTGAGTTGCC 1059  
Db 1064 GTGCTATGTCATCAAGAACTGTATTTTGAAGGCACTGACATGATCGAGAAGTTGCC 1123  
Qy 1060 TTATGATGCTCATGGCTTACCTTTCAVATATGCTGGCTGAGTTGCTAGATTTGAGCGGCA 1119  
Db 1124 TCATGATGCTTATGGCTTATCTTTCATATATGCTTGTGAGTATTCGCTTGAATGTTA 1183  
Qy 1120 TTTCTACCGTATCTTCTGCGGTATTTGATGTCACATTAACATTTGAGTGCATTAACGTACAG 1179  
Db 1184 TCCTAACTGTATTTTCTGTGGGATTTGTGATGTCCTCCATTAACATTTGCAAAATGTCA 1243  
Qy 1180 AGAGTCTAAGAGTTTACAAACAGCAGCACTTTGCAACTCTGCTCTTCAATTTGCTGAGACT 1239  
Db 1244 AGAGTCTAAGAAATTAACCAAGCATGCTTTGCTATTTGCTGTTTCTCGCTGAGACT 1303  
Qy 1240 TTTCTTCTCTGATGTTGGGATGATGCAATTTGATATTTGAAAAATGGGAGTTTGCAGTG 1299  
Db 1304 TTAATTTCTCTCTAGTTGGATGATGCAATTTGGACATAGAGAAATGAGATTCGTGAGTG 1363  
Qy 1300 ACAGACTGGCAATTCATTTGGGATTAAGCTCAATTTTCTAGGATTTGGTCTGATTTGGA 1359  
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Qy 1540 ATGCAATAATGATCACCAGACCACTACATGCTGTTCTTTTATGACATATGTAATTTGGGA 1599  
Db 1604 ATGCAATCATGATTAACCACTGATTAATACCTTAATGCCACACCAAAAGCGACAGTACCA 1663  
Qy 1600 TGATGACAAAGCAATGATCAGGCTGCTGTAC-----CGGCTTCAGGCC 1644  
Db 1664 TGCTAACCAACCACTGATTAATACCTTAATGCCACACCAAAAGCGACAGTACCA 1723  
Qy 1645 ATCTGTGCTGAGCTTCAATCACCAGAGTCCCTGCAATTTCTCTCTCTGACAGCA 1704  
Db 1724 CGAGTATGTTATCGGACGATAGCACTCCGAAATCAATTCACATTCGCTCTCTCGATGGT 1783

Qy 1705 TGCAGAGTTTCTGACCTCGAGAGTACAACA-----ACATTGTGAGGCTTCCAGCC 1755  
Db 1784 RACACCTAGATTCAATTTGAGTTTACCTGGGAGCCACAGGACGTGCCACCAACAGCC 1843  
Qy 1756 TCCGATGCTCTCTACCAAGCGGACCCACACTGCTACTACTTGGCGCAAGTTGAGG 1815  
Db 1844 TTCGAGGTTTCTCTATGCGCCCCACACAGGACTGCTCACTATTACTGGAGACAGTTTGATG 1903  
Qy 1816 ACGCGCTGATGCGACCGATGTTTGGCGGCGGGTTCGTCCCTTCTCCCTGATCAC 1875  
Db 1904 ATGCTTTCAAGGCTCTGTGTTGTGCGGATTCGTTCCCTTGTCTGCTGTTCTC 1963  
Qy 1876 CAACGAGCAGAGC 1889  
Db 1964 CGACTGAGAGAGC 1977

RESULT 3  
US-10-155-535-3  
; Sequence 3, Application US/10155535  
; Publication No. US20030046729A1  
; GENERAL INFORMATION:  
; APPLICANT: Blumwald, Eduardo  
; APPLICANT: Apse, Maris  
; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY  
; FILE OF INVENTION: EXPRESSION OF VACUOLAR CATION-PROTON ANTIPORTERS  
; FILE REFERENCE: 52915200720  
; CURRENT APPLICATION NUMBER: US/10/155,535  
; CURRENT FILING DATE: 2002-05-24  
; PRIOR APPLICATION NUMBER: 09/271,584  
; PRIOR FILING DATE: 1999-03-18  
; PRIOR APPLICATION NUMBER: 60/078,474  
; PRIOR FILING DATE: 1998-03-18  
; PRIOR APPLICATION NUMBER: 60/116,111  
; PRIOR FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 2066  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-155-535-3

Query Match 30.5%; Score 711; DB 9; Length 2066;  
Best Local Similarity 65.8%; Pred No. 7, 7e-212;  
Matches 1054; Conservative 0; Mismatches 540; Indels 9; Gaps 1;

Qy 343 CCTCCGACTACGCTCGGTGGTGTCCATCAACCTGTTCGTGCGGTGCTCTGCGCTGCA 402  
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Qy 403 TGTCTCTCGGCACCTCTCGAGGAGATCGTGGGTCAATGAGTCCATCACCAGGCTCA 462  
Db 110 TCGTGTGTTGTTGCTTGTCTGAGGAGACTCGGTGGATGAACGAGTCAATCTGCTCTTA 169  
Qy 463 TCATCGGCTCTGCAACCGGCTGGTGTCTGCTGATGACCAAGAGAGAGCTCGCACT 522  
Db 170 TCAATGGTTCGTGTACTGAGATTTGTAUCTGCTTATAGTGGAGGCAAAAGCTCAAGA 229  
Qy 523 TATTCGTTTCAGTGAGGATCTCTTTCTTCATCTACCTCTCCCTCGATCATCTTCAATG 582  
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Qy 643 GAGCGTTCGGGCAATGATATCTTTTTCACAAATATCTATTTGCTGCAATTTGCAATTTCA 702  
Db 350 GTGCTATTGGAATCTCTCAATTTTCAATTTGTTTATCTATCTATTTGTTGCTAAACATCTTT 409  
Qy 703 GCAGATGAACATTTGGAACGCTGGATGTAGGAGATTTTCTTCAATTTGGAGCCATCTTTT 762

Db 410 AGAAATGAATATCGGTGATCTTACCATTTGGGAGTATCTAGCCATTTGGAGCAATATTCT 469  
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Qy 823 ACAGTCTGGTATTCGGTGAAGGTGTGTGAACGATGCTACATCAATTTGTGCTTTTCAACG 882  
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Qy 883 CACTACAGAACTTTGATCTTGTCCACATAGATGCGGCTGTCTGAAATTTCTTTGGGA 942  
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Qy 943 ACTTCTTTATTTATTTTGTGAGCACCTCTCTTTGGAGTATTTCTGCTGATTTGCTCAGTG 1002  
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Qy 1003 CATACATCAAGAGCTTATACATTTGAAGGCACTTCTACTGACCGTGAAGTTGCCCTTA 1062  
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Qy 1123 TCACCGTATCTTCTGTGATTTGATTAATGTACATTTGACATTAACGTCACAGAGA 1182  
Db 830 TGACTGTGTTCTTCTGCGGATTTATATGTTCTACATATACATGGCACAATGTTACAGATA 889  
Qy 1183 GTTCAAGAGTTACAAACAAAGCAGCATTTGCAACTCTGTCTTCAATTTGCTGAGACTTTTC 1242  
Db 890 AATCAAGGTCACTACAAAACATCTTTTGTGCAATGTCAATTTCTAGCTGAGATTTTGA 949  
Qy 1243 TCTTCTCTATGTTGGATGATGATTTGATATGATTTGAAATGGAGTTTGGCAGTGACA 1302  
Db 950 TCTTCTTATGCTTGAATGAGCGCTCTCGATATCGAATAATGGAGCTTTGTACGCAACA 1009  
Qy 1303 GACCTGGCAAAATCCATTTGGGATAAGCTCAATTTTCTAGGATTTGTTCTGATTTGGAAGAG 1362  
Db 1010 GTCTGTGTCAGTGTGATGAGTGTAGTTCAATCTTCTTTGGGCTTATCTTCTGGTCTCGC 1069  
Qy 1363 CTGCTTTTGTATTCCTGCTGTGTTCTGTGAACTTCAAAAGGCTTCAACCGGATGAGA 1422  
Db 1070 CCGGCTTCTGTTTCCACTTCTTCTTGTCCAATTTAAACAAAGTCTTCAACCGGATGAGA 1129  
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Qy 1483 CGATTGCTTCTGTCTTACAAATAGTTTACAAGATCTGGCCATCTCAGCTGCACGGCAATG 1542  
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Qy 1603 TGACAAAGCCATGATCAGGCTGCTGCTACCGGCTCAGGCATCTCTCACTCTGAGC 1662  
Db 1310 TAAACAAACCGTTAGTCAAAATTTTGGAGCTTCTATCAAAACAGTCTCCACGACCGCGC 1369  
Qy 1663 -----CTTCATCACCAGTCCCTGCAATTTCTCTCTCTGCAAGCATGGAAGTT 1713  
Db 1370 TGCAGATCACACTAAGATCTTCTTCCAGATCCGATCTCCATGAGCGGTTGTCAGTA 1429  
Qy 1714 CTGACCTCGAGAGTACAAACCAATGTGAGGCTTCCAGGCTCCGATGCTCTCACCA 1773  
Db 1430 CCCAAGGCCAGTCAGAAATACCAACCCCTGAACCAACATGTTAGCTTCAGAAATGTTCTGGAAT 1489  
Qy 1774 AGCCGACCCACACTGCTCCACTACTACTGCGCAAGTTTCGACGCGCTGATGCGACGA 1833

Db 1490 CTCGCTCAGGCGCATTCATCTACTGAGGAAATTCGATAACGCACTTATGCTCGCA 1549  
Qy 1834 TGTTTGGCGGCGGGGTTCTGTCGCTTCTCCCTGGATCAACCAACGAGAGCCCATG 1893  
Db 1550 TATTTGGTGGCGAGGCGTTTCCAGTAGTTCCAGGTTTCAACCATTTAGAAATAGTGTTC 1609  
Qy 1894 GAGGAAGATGAACAGTGCAGAAAGAAATGAGAAATGGAATGGATGTTGA 1936  
Db 1610 CGCAATGGAGTGAAGAGTAGAAAAACAGGAACAAACGCGGA 1652

RESULT 4  
US-09-294-093B-2697  
; Sequence 2697, Application US/09294093B  
; Patent No. US20010051335A1  
; GENERAL INFORMATION:  
; APPLICANT: Lalgudi, Raghunath, V.  
; APPLICANT: Ito, Laura, Y.  
; APPLICANT: Sherman, Bradley, K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL  
; FILE REFERENCE: PL-0009 US  
; CURRENT APPLICATION NUMBER: US/09/294,093B  
; CURRENT FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: 60/082,567  
; PRIOR FILING DATE: April 21, 1998  
; NUMBER OF SEQ ID NOS: 6207  
; SOFTWARE: PERL Program  
; SEQ ID NO 2697  
; LENGTH: 281  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700346512H1  
; NAME/KEY: unsure  
; LOCATION: 2  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-294-093B-2697

Query Match 6.0%; Score 138.8; DB 10; Length 281;  
Best Local Similarity 72.5%; Pred. No. 5.3e-33;  
Matches 208; Conservative 0; Mismatches 73; Indels 6; Gaps 2;  
Qy 1029 GGAAGGCACTTCTACTGACCGTGAAGTTGCCCTTATGATGCTCATGGCTTACCTTTCAAT 1088  
Db 1 GNCAGACATTCACTGATAGAGAGTTTCTATCATGATACTCATGGCATACTTTCATAC 60  
Qy 1089 ATGCTGGCTGAGTTGCTAGATTGAGCGGCATTTCTACCGTATTTCTTCTGTGGTATTGTA 1148  
Db 61 ATGATATCAATGCTGTGAGACCTGAGTGAATTTCTTACTGTCTTCTTCTGTGGAAATGTA 120  
Qy 1149 ATGTCACATTACACTTGGCATAACGTCACAGAGATTCAAGAGTTACAACAAAGCAGCA 1208  
Db 121 ATGTCACATTACACTTGGCATAATGTGACAAAGTTCTAGGGTTACCAACAGCATACT 180  
Qy 1209 TTTGCAACTCTGTCTTCTTCTTCTGCTGAGACTTTTCTTCTCTGTATGTTGGATGGATGCA 1268  
Db 181 TTTGCAACTT-----ATCATCATGCAGAAATTTCTCTCTCTATGTTGGATGGATGCA 236  
Qy 1269 TTGATATTGAAATATGGGAGTTTGGCAGTGACAGACTTGGCAATC 1315  
Db 237 T--GGACATGAGAGTGGAAATAGCTAGTAGCAGTCTTAAGAAACC 281

RESULT 5  
US-10-155-535-5  
; Sequence 5, Application US/10155535  
; Publication No. US20030046729A1  
; GENERAL INFORMATION:  
; APPLICANT: Blumwald, Eduardo  
; APPLICANT: Apse Maris  
; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY  
; EXPRESSION OF VACUOLAR CATION-PROTON ANTI-PORTERS





Db 3779 GCAACTGATCCAGTACGTTCTTCTGCTATATTCACAGAGCTTCAAGTGTGATGTTGAACATC 3720  
Qy 822 TACAGTCTGGTATTCGGTGAAGGTGTGTGAACAGATCTACATCAATTTGCTTTTCAAC 881  
Db 3719 TATGCACTTCTTTTGTGAAGGTCTCTCAATGATGCTGTTCGCCATGCTGTCTCC 3660  
Qy 882 GCACTACAGAACTTTGATCTTG-----TCCACATAGATGGCGTGTGCTT 926  
Db 3659 TCAATAGTGGCATACCAAGCCAGCTGGAGACAACAGTCAACACCTTTGATGTCACAGCGATG 3600  
Qy 927 CTGAAATCTTGGGAACCTCTTTTATTTATTTTGTGCGAGCACCTTCCCTTGGAGTATTT 986  
Db 3599 TTCAAGTCTATTTGGATTTCTTCTTGGAACTCTTCAGTGAATCTTTGCAATGGGTGCTGCT 3540  
Qy 987 GCTGGATTGCTCAGTGCATACATAATCAAGAAGCTATACATTTGGAAGGCATTTACTGTAC 1046  
Db 3539 ACTGGAGTGGTACAGCTT---TAGTCACAAAGTTTACCAAAATTTACGGAGTTCCAGTTG 3483  
Qy 1047 CGTGAGTGTGCTTATGATGCTCATGGCTTACCTTTTCATATATGCTGGCTGAGTTGCTA 1106  
Db 3482 TTGGAGACAGGCTGTCTTCTTCTGATGCTCCTGGAGTACCTTCTCTTGGCTGAAGCATGG 3423  
Qy 1107 GATTTGAGCGCATCTCACGGTATCTCTGTGTTATTTGATGTCACATTTACACTTGG 1166  
Db 3422 GCGTTACAGGTGATGTTGCGATATTTGTTTGGCATCACAAAGCACATTTATACGTAT 3363  
Qy 1167 CATAACGTACAGAGTTCAGAGTTTACAAAGCAGCATTTGCAACTCTGTCTCTTC 1226  
Db 3362 AATAATTTGTCACGGAGTCTCAGCATAGAACTAACAAGTTTGTAGCTTCTCAATTTTC 3303  
Qy 1227 ATTCTGAGACTTTTCTCTCTCTGATATGTTGGGATG 1262  
Db 3302 TTGGCAGAGAAATTCATCTTCTCTCTACATGGGGCTG 3267

## RESULT 9

US-09-800-729-58  
; Sequence 58, Application US/09800729  
; Patent No. US2002068319A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: 32 Human secreted proteins  
; FILE REFERENCE: PZ044P1  
; CURRENT APPLICATION NUMBER: US/09/800,729  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: PCT/US00/26013  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 60/155,709  
; PRIOR FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 58  
; LENGTH: 1354  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-800-729-58

Query Match 2.2%; Score 52.4; DB 10; Length 1354;  
Best Local Similarity 52.8%; Pred. No. 2.2e-05;  
Matches 113; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy 1050 GAGGTGTGCTTATGATGCTCATGGCTTACCTTTTCATATATGCTGGCTGAGTTGCTAGAT 1109  
Db 18 GAGACGGCGCTGTTCTTCTCTCATGCTCTGGAGCAGGTTCTTGGCAGAGCCCTGGCGA 77  
Qy 1110 TTGAGCGGCATCTCACCGTATTTCTTGTGTTATTTGATGTCACATTTACCTTGGCAT 1169  
Db 78 TTTACAGGTGTTGATGCTGCTCTTCTGTTGGAATTCACAAAGCTCATTTACACCTACAAC 137  
Qy 1170 AACGTCACAGAGTTCAGAGTTTACAAAGCAGCATTTGCAACTCTGTCTCTTCATT 1229  
Db 138 AATCTGTCTGGTGAATCAAGAAGTCGAACCAAGCAGCTCTTTTGAGGTGTACATTTCTCTG 197

Qy 1230 GCTGAGACTTTTCTCTCTCTGATGTTGGGATGG 1263  
Db 198 GCAGAGAACTTCTCTCTCTACATGCGGCTGG 231

## RESULT 10

US-10-217-096-3  
; Sequence 3, Application US/10217096  
; Publication No. US2003004493A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Roy A. J., Perriera, Holly M.  
; TITLE OF INVENTION: 96895, A Human Sodium-Hydrogen Exchanger  
; TITLE OF INVENTION: Family Member and Uses Therefor  
; FILE REFERENCE: MP101-147P1RM  
; CURRENT APPLICATION NUMBER: US/10/217,096  
; CURRENT FILING DATE: 2002-08-12  
; PRIOR APPLICATION NUMBER: 60/312,544  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1935  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1935)  
US-10-217-096-3

Query Match 2.2%; Score 51.4; DB 9; Length 1935;

Best Local Similarity 46.2%; Pred. No. 5.9e-05;  
Matches 350; Conservative 0; Mismatches 371; Indels 36; Gaps 4;

Qy 540 GATCTCTTCTCTCATCTACCTCTCTCTCTCTCAATTCAGTGGTTCAGGTAAAG 599  
Db 394 GAAATCTTCTCTCAATGTTTACTGCCACCAATATATTTTCAGGATATAGTCTAAAG 453  
Qy 600 AAAAAAGCAATTTCCGGAATTTTCATGACGATTCATATTTTGGAGCCGCGGCAATG 659  
Db 454 AAGAGACACTTTTTCAAAACCTTAGGATCTATTTTAAAGTATGCTCTTCTGGAACTGCC 513  
Qy 660 ATATCTCTTTTTCACATA-----TCTATGCTGCCATTCGATATATTC 701  
Db 514 ATCTCTCTGATCGTCTATAGGTTAATATGATGTTTGTGAAGGCTATGATCATGCT 573  
Qy 702 AGCAGAAATGAACATTTGGAACGCTGGATGTAGGAGATTTTCTTGCATTTGGAGCCATCTTT 761  
Db 574 GGGCAGCTGAAAAATGGAGACTTTTCATTTCTGACTGTTTATTTTGTGTTTCACTGATG 633  
Qy 762 TCTGCGACAGATTTCTGCTGCACTTGGAGGTCCTCAAT---CAGGATGAGACACCTTTT 818  
Db 634 TCTGCTACAGATCCAGTGCAGTGTGCTGCTGCTTTCATGAACTGCACTGCACTGCACTGAC 693  
Qy 819 TTGTACAGTCTGTTATTCGGTGAAGGTGTTGGAAGGATGCTACATCAATTTGCTGCTTTC 878  
Db 694 CTGTACACACTCTTGTGTTGGAGAGATGTTGTTGAATGATGCTGCTGCTGCTGCTTACA 753  
Qy 879 AAGCAGCTACAGAACTTTGATCTTGTCCACA-----TAGATCGGCTGCTGCTT 926  
Db 754 TATTCTATATCCATTTTACAGTCCCAAGGAGATCCAAATGCAATTTGATGCGCAGCATTC 813  
Qy 927 CTGAAATCTTGGGAACCTTTCTTTTATTTTATTTTGTGAGACACCTTCTTGTGAGTATTT 986  
Db 814 TTCCAGTCTGTGGGAAATTTCT---GGGAATCTTCTGCTGCTCATTTGCAATGGGCTCT 870  
Qy 987 GCTGGATTCCTCAGTGCATACATAATCAAGAAGCTATACATTTGGAAGGCAATTTCTACTGAC 1046  
Db 871 GCGTATGCCATCATCACAGCACTGTTGACCAAAATTTACCAAGCTGTGTGAGTTCGCGATG 930  
Qy 1047 CGTGAGGTTGCCCTTATGATGCTGCTTACCTTTTCATATATGCTGCTGCTGCTGCTA 1106  
Db 931 CTGGAACCGGCTGTTTCTTCTGCTTCTTGTGAGTGCCTCTCTGCTGCGAGGCTGCC 990

QY 1107 GATTGAGGCAATCTCACCCTATTTCTTCTGTGTATTTGTAATGTCAATTAACACTTGG 1166  
Db 991 GGCCTAACAGGATAGTTGCTCTTCTTCTGTGGAGTACACAAGCACATTAACCTAC 1050  
QY 1167 CATACAGTCACAGAGATTCAAGAGTTACAACAAGACGCAATTTGCAACTCTGCTTC 1226  
Db 1051 AACATCTGTCTTCGGAATCCAAAATAAGAACTAAACAGTTGTTGAATTTATGAACATT 1110  
QY 1227 ATTGCTGAGACTTTTCTTCTCTGTATGTTGGATGG 1263  
Db 1111 TTGGCGGAGAACGTCACTCTCTGTATCATGGGCTGG 1147  
RESULT 11  
US-10-217-096-1  
; Sequence 1, Application US/10217096  
; Publication No. US20030044933A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J., Ferriera, Holly M.  
; TITLE OF INVENTION: 96895, A Human Sodium-Hydrogen Exchanger  
; FILE REFERENCE: MPI01-147P1RM  
; CURRENT APPLICATION NUMBER: US/10/217,096  
; PRIOR FILING DATE: 2002-08-12  
; PRIOR APPLICATION NUMBER: 60/312,544  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3537  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (82)...(2016)  
US-10-217-096-1

Query Match 2.2%; Score 51.4; DB 9; Length 3537;  
Best Local Similarity 46.2%; Pred. No. 9.2e-05;  
Matches 350; Conservative 0; Mismatches 371; Indels 36; Gaps 4;

QY 540 GATCTCTTCTCATCTACTCTCCTCCGATCATCTTCAATGCAAGTTTTCAGGTAAAG 599  
Db 475 GAAATCTTCTTCAAGTTTATCTGCGCAATATATTTTCAGGAGATATAGTCTAAAG 534  
QY 600 AAAAGCAATTTCTCCGAAATTCATGACGATCAATTTATTTGGAGCGCTCGGACAAATG 659  
Db 535 AAGACACATTTTTCAAAACCTTAGGATCTATTTAAAGTATGCTTCTTGGAACTGCC 594  
QY 660 ATATCTTTTTCACAATA-----TCTATGTGTCGCAATTCGAATATTC 701  
Db 595 ATCTCTCGATCGTCATAGGGTTAATTTATGATGTTTGTGAAGCTATGATACATGCT 654  
QY 702 AGCAGATGAACATTTGGAACGCTGGATGAGATTTTCTTGCAATTTGGAGCAATCTTT 761  
Db 655 GGCCAGCTGAAAAATGGAGACTTTCATTTCACTGACTGCTTTATTTTGGTTCATGATG 714  
QY 762 TCTGCGACAGATTTCTGTCGACATTTGAGGTCTCAAT---CAGGATGAGACACCTTT 818  
Db 715 TCTGTACAGATCAGTACAGATGCTGCCATTTTCCATGAACTGCAGCTGCACCTGAC 774  
QY 819 TTGTACAGCTGGTATTCGGTGAAGGTTGTGTAACGATGCTACATCAATTTGTGCTTTTC 878  
Db 775 CTGTACACACTCTTGTGAGAGAGAGTGTGTAATGATGCAAGTGGCCATAGTCTCTTACA 834  
QY 879 AACCACCTACAGAACTTTGATCTTGTCCACA-----TAGATGGGCTGTGCTT 926  
Db 835 TATTCATATCCATTTACAGTCCCAAGAGAAATCCAAATGCAATTTGATGCGCGACATTC 894  
QY 927 CTGAAATCTTTGGGAACTCTTTTATTTATTTTGTTCGACACCTTCTTGGAGTATTT 986  
Db 895 TTCCAGTCTGTGGGAATTTTCT---GGGAATCTTCGCTGCTCATTTGCAATGGGCTCT 951

QY 987 GCTGATGTCTCACTGATACATAATCAAGAAGCTATACATTTGGAAGCAATTTCTACTGAC 1046  
Db 952 GCGTATGCCATCATCACAGCACTGTTGACCAAAATTTACCAAGCTGTGTGAGTTCCCGATG 1011  
QY 1047 CGTGAGGTGGCCCTATGATGCTCATGGCTTACCTTTTATATATATGCTGGCTGAGTTGCTA 1106  
Db 1012 CTGAAACCCGCCCTGTTTTCCTCTCTTCTTGGAGTGCCTTCTCTGCGGAGCTGCC 1071  
QY 1107 GATTGTAGCGGCATTTCTCACCGTATTTCTTGTGTGTTATTTGTAATGTCAATTAACACTTGG 1166  
Db 1072 GGCCTAACAGGATAGTTGCTGTTCTCTTCTGTGAGTACACAAGCACATTAACCTAC 1131  
QY 1167 CATACAGTCACAGAGATTCAAGAGTTACAACAAGACGCAATTTGCAACTCTGCTTC 1226  
Db 1132 AACAACTGTCTTCGGATTTCCAAAATAAGAACTAAACAGTTGTTGAATTTATGAACATT 1191  
QY 1227 ATTGCTGAGACTTTTCTTCTCTCTGTATGTTGGATGG 1263  
Db 1192 TTGGCGGAGAACGTCACTCTCTGTATCATGGGCTGG 1228

## RESULT 12

US-09-815-242-7730  
; Sequence 7730, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; TITLE OF INVENTION: Prokaryotes  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7730  
; LENGTH: 1305  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1305)  
US-09-815-242-7730

Query Match 1.9%; Score 44.4; DB 10; Length 1305;  
Best Local Similarity 46.2%; Pred. No. 0.0069;  
Matches 147; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

QY 299 GGGGATGGAGTGGCGCGCGGCTTGTACACGACCTCCGACTACGGCTC 358  
Db 726 GGTGAAGAGCTGTTCCTCCGAGCGCAGCGGTACTCTGACGACCAACGAGCT 785  
QY 359 GGTGGTGTCCATCAACCTGTTGCTGCGCTGCTGTGCGCTGATGCTCTCGGCCACCT 418



Db 786 GCTCGGCGCGCTCGGTGTTCGCCCATGCTGCGACCTGCGGCAATGCCAGCG 845  
Qy 419 CCTCGAGAGATCGCTGGGTCAATGATCCATCACCGCGCTCATCATCGGGCTCTGCAC 478  
Db 846 CCTGGCGAGAGCTGCTGCGCGGTGGGTTCCTGCCGACCTCCAACTGTTCTCTCGGCG 905  
Qy 479 CGGCGTGTGATCTGCTGATGACCAAGGAAGAGCTGCGACTTATTCTCTTCAAGTGA 538  
Db 906 CGGTCTGTTCGACCTCGGAGCTGGAGCTACAAAGTCAAGTTCGGCTCGGACCGA 965  
Qy 539 GGATCTCTTCTTATCTACCTCTCCCTCCGATCACTTCAATGACAGTTTTCAGGTAAA 598  
Db 966 TGTGCGGCGCGGACCACTCTCTCCAGCTGCTCCAGCTGCTGAGCGGCTGACAAAGTTCAT 1025  
Qy 599 GAAAAAGCAATCTTCCG 616  
Db 1026 GCAATTGAGGGCGCGG 1043

## RESULT 13

US-10-033-109-9

; Sequence 9, Application US/10033109

; Patent No. US20020142390A1

; GENERAL INFORMATION:

; APPLICANT: Allen, Stephen M.

; APPLICANT: Rafaleki, J. Antoni

; APPLICANT: Sakai, Hajime

; TITLE OF INVENTION: Nitrogen Transport Metabolism

; FILE REFERENCE: BB-1210

; CURRENT APPLICATION NUMBER: US/10/033,109

; PRIOR FILING DATE: 2001-12-28

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248

; PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 9

; LENGTH: 1883

; TYPE: DNA

; ORGANISM: Oryza sativa

US-10-033-109-9

Query Match 1.8%; Score 43.4; DB 12; Length 1883;  
Best Local Similarity 47.3%; Pred. No. 0.019;  
Matches 131; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

Qy 296 CATGGGATGGAGGTGGCGGCGGCGGCTGGGGGCTGTGTACACGACCTCCGACTACGC 355  
Db 524 CACGCTGTGTCTGCTCGCGGGTCTCTCGGGAGGATGAACATCAAGGCGTGATGGC 583  
Qy 356 GTCGCTGTGTTCATCAACCTGTGCTGCTGCGCGCTGCTGCGCGCTGATGCTCTCGGCCA 415  
Db 584 GTTCACTCGCTCTGGCTCTCTTCTCTACACCGCTCTGCGCGCTTACGCTCTGGGGCGG 643  
Qy 416 CCTCTCGAGGAGATCGCTGGTCAATGAGTCCATCACCGCTCATCGGCGCTCTG 475  
Db 644 CGGCTTCTCTACCAAGTGGGGGCTCATGCTACTTCCGGGGATACGTCATCCACCTCTC 703  
Qy 476 CACCGCGTGTGTGATCTTGTGATGACCAAGGAAGAGCTCGCACCTTATTCTCTTCAG 535  
Db 704 CTCGGGATCGCGGCTTACCGCGGCTACTTGGGTGGGGCGGAGGCTGAGAGCGACAG 763  
Qy 536 TGAGGATCTTCTTTCATCTACCTCTCTCCCTCCGATC 572  
Db 764 GGAGCGGTCTCGCGGAACAACATCTCTCTCATGATC 800

## RESULT 14

US-09-887-576-816

; Sequence 816, Application US/09887576

; Patent No. US20020144047A1

; GENERAL INFORMATION:  
; APPLICANT: Budworth, P.  
; APPLICANT: Brown, D.  
; APPLICANT: Chang, H.  
; APPLICANT: Zhu, T.  
; APPLICANT: Han, B.  
; APPLICANT: Wang, X.  
; APPLICANT: Cooper, Bret  
; TITLE OF INVENTION: Promoters for regulation of plant expression  
; FILE REFERENCE: 1360.001US1  
; CURRENT APPLICATION NUMBER: US/09/887,576  
; CURRENT FILING DATE: 2001-06-25  
; PRIOR APPLICATION NUMBER: US 60/213,848  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/214,087  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/258,692  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 875  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 816  
; LENGTH: 690  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
US-09-887-576-816

Query Match 1.8%; Score 43; DB 10; Length 690;

Best Local Similarity 49.3%; Pred. No. 0.012;

Matches 112; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 262 CGGTGGTGGCGGAGAAAGTCCCGCTGAGGATGGGATGAGGTGGCGGCGGC 321  
Db 71 CGCTGGCGGCTCTGTGGTGGTGGCGCTGGCGCAACGCGTGGCGGCGCGG 130  
Qy 322 GCGTGGGCGCTCTGTACAGCACTCGGACTAGCGTGGTGGTGGTCCATCAACCTGTCG 381  
Db 131 TGGCGGTTTTCGCGCAACGCTTCGGCGGCGGCACTCAACCGGCGCTCAGTTCCGCGTGC 190  
Qy 382 TCGCGCTGCTGCGCGCTGCATCGTCTCGGCGCACTCTCGAGGAGAATCGCTCGGTCGA 441  
Db 191 TGTGCGGCGCGCATCTCTTCTCGCGCGCGCGGCTCTACTGGCGCGCCAGCTGCTCG 250  
Qy 442 ATGAGTCCATCACCGCGCTCATCATCGGCTCTGACCGGCGGTGTG 488  
Db 251 GCGCGTGTCTGCGCGTGTCTCTCTCTCAGGCTGGCTCGCGAGGCATG 297

## RESULT 15

US-10-040-739-929

; Sequence 929, Application US/10040739

; Patent No. US20020173635A1

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth

; McCoy, John

; LaVallie, Edward

; Racie, Lisa

; Merberg, David

; Treacy, Maurice

; Spaulding, Vikki

; TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS

; NUMBER OF SEQUENCES: 1519

; CORRESPONDENCE ADDRESS:

; ADDRESS: Genetics Institute, Inc.

; STREET: 87 Cambridgepark Drive

; CITY: Cambridge

; STATE: Massachusetts

; COUNTRY: U.S.A

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

Search completed: April 5, 2003, 17:54:07  
Job time : 223 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 12:22:03 ; Search time 3711 Seconds

(without alignments)  
10168.549 Million cell updates/sec

Title: US-09-888-035A-1

Perfect score: 2330

Sequence: 1 gagaagagagattttgtagc.....ttgaaaaaaaaaaaaaaaaa 2330

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estmu.\*

5: em\_estov.\*

6: em\_estpi.\*

7: em\_estro.\*

8: em\_htc.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_htc.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: gb\_gss.\*

18: em\_gss\_hum.\*

19: em\_gss\_inv.\*

20: em\_gss\_pln.\*

21: em\_gss\_vrt.\*

22: em\_gss\_fun.\*

23: em\_gss\_man.\*

24: em\_gss\_mus.\*

25: em\_gss\_othr.\*

26: em\_gss\_pro.\*

27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	827.4	35.5	2080	11 AY105332	AY105332 Zea mays
2	745.8	32.0	3272	11 AY109416	AY109416 Zea mays
3	656.8	28.2	711	9 AU094795	AU094795 AU094795
4	566	24.3	719	13 BJ312595	BJ312595 BJ312595
5	473.2	20.3	1212	10 BE420587	BE420587 HWM000.D1
6	412.2	17.7	690	14 BQ865196	BQ865196 QGC2a03.Y

7	400.6	17.2	665	13 BI933988	BI933988 EST553877
8	396	17.0	632	13 BJ316128	BJ316128 BJ316128
9	390.2	16.7	802	14 BQ512490	BQ512490 EST619905
10	366.6	15.7	733	14 BU004460	BU004460 QG5E06.Y
11	362.8	15.6	607	14 BQ612167	BQ612167 sap80d01.Y
12	361	15.5	666	14 BQ163913	BQ163913 952081B08
13	359.4	15.4	638	13 BJ317459	BJ317459 BJ317459
14	343.6	14.7	637	13 BM109451	BM109451 EST556987
15	340.4	14.6	378	14 C91832	C91832 C91832 Rice
16	334	14.3	621	13 BM660526	BM660526 952039C06
17	329.8	14.2	637	13 BM660977	BM660977 952043D06
18	319.4	13.7	706	13 BJ291707	BJ291707 BJ291707
19	311.4	13.4	685	14 BQ969464	BQ969464 QH838G07.Y
20	303.4	13.0	646	14 BQ996834	BQ996834 QG613018.Y
21	303.2	13.0	553	14 BQ034865	BQ034865 1091010A0
22	298.4	12.8	486	9 AI938253	AI938253 sc41h02.Y
23	297.2	12.8	502	10 BE440835	BE440835 sp42f03.Y
24	287.2	12.3	834	11 AV110110	AV110110 Zea mays
25	276.6	11.9	484	9 AL822495	AL822495 AL822495
26	266.4	11.4	653	10 AW685820	AW685820 NF035E04N
27	262	11.2	697	14 BQ508685	BQ508685 EST616100
28	261.6	11.2	619	10 AV909979	AV909979 AV909979
29	261.4	11.2	793	14 BQ504663	BQ504663 EST612066
30	252.6	10.8	469	10 BE643915	BE643915 NXCI 048
31	249.6	10.7	424	10 AV408114	AV408114 AV408114
32	249.2	10.7	515	13 BM660527	BM660527 952039C06
33	247.8	10.6	693	14 BU007951	BU007951 QGH5P21.Y
34	234.8	10.1	452	12 BG464161	BG464161 EMI 70 D0
35	228.6	9.8	663	14 BQ999928	BQ999928 QGG23H02.Y
36	225.8	9.7	639	13 BI176128	BI176128 EST517211
37	225.2	9.7	515	12 EG649564	EG649564 EMI 80 H0
38	220.2	9.5	651	14 C99909	C99909 C99909 Arab
39	218.6	9.4	556	10 BE600656	BE600656 PII 91 A1
40	218.2	9.4	565	14 BQ163719	BQ163719 952081B08
41	215.2	9.2	464	10 BE498756	BE498756 WHE0965 C
42	211.4	9.1	562	14 BQ696274	BQ696274 NXFV 037
43	210.2	9.0	401	10 BE607262	BE607262 NXCI_034
44	206.2	8.8	565	9 AL818407	AL818407 AL818407
45	203.4	8.7	698	10 BE597324	BE597324 PII_72_A1

# ALIGNMENTS

RESULT 1

AY105332	AY105332	Zea mays	PC0131050	mRNA	linear	HTC 25-MAY-2002
LOCUS	AY105332	Zea mays	PC0131050	mRNA	linear	HTC 25-MAY-2002
DEFINITION	AY105332	Zea mays	PC0131050	mRNA	linear	HTC 25-MAY-2002
ACCESSION	AY105332	Zea mays	PC0131050	mRNA	linear	HTC 25-MAY-2002
VERSION	AY105332.1	GI:21208410				
KEYWORDS	HTC.					
SOURCE	Zea mays.					
ORGANISM	Zea mays.					
REFERENCE	1 (bases 1 to 2080)					
AUTHORS	Hayney,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.					
TITLE	Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes					
JOURNAL	Unpublished (2002)					
REFERENCE	2 (bases 1 to 2080)					
AUTHORS	Coe,E.C.					
TITLE	Direct Submission					
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA					
FEATURES	Location/Qualifiers					
source	1..2080					
	/organism="Zea mays"					
	/db_xref="MaizeDB:637649"					
	/db_xref="taxon:4577"					
	/clone="PC0131050"					

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/clone\_lib="Maize Mapping Project/DuPont Consensus Library"

/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

BASE COUNT 483 a 505 c 471 g 621 t  
ORIGIN

Query Match 35.5%; Score 827.4; DB 11; Length 2080;  
Best Local Similarity 69.9%; Pred. NO. 3e-164;  
Matches 1130; Conservative 0; Mismatches 486; Indels 1; Gaps 1;

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Qy 273 CGGAGAAGTCGCGCGGTGAGGATGGGATGGAGGTGGCGGCGCGGTGGGGCT 332
Db 163 CGGTGGATCTCTGGGTGGGACATGGCCCTGGGTGGGAGCTCTTCAAAATCCGGC 222
Qy 333 CTGTACACGACCTCCGACTACGCGTCGCTGCTGTCATCAACCTGTTGCTCGCGCTGCTC 392
Db 223 GGGCTCTCGGTCTCGGATCAGACGCCATCGTCTCGATTAACATCTTCAATCGCGTCTC 282
Qy 393 TCGCGCTGATCGTCTCGGACCTCTCGAGGAGATCGCTGGGTCAATGAGTCCATC 452
Db 283 TGCAGCTGCATTTGATCGGCCACTTGTGGAAGGGAACCGATGGGTGAACGAGTCCATC 342
Qy 453 ACCGCGCTCATCATCGGCTCTGACCGCGGTGATCTTCTGCTGATGACCAAGGGAAG 512
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Qy 513 AGCTCGCACTTATTCGTTCTCAGTGAGGATCTCTTCTTCTCATCTACTCTCTCCCTCCGATC 572
Db 403 AACTCACGATCTTGTGTTGTCAGCGAGACCTGTTTTCATATATTTACTTCCGCGATA 462
Qy 573 ATCTTCAATGCAAGTTTTCAGTAAAGAAAGCAATTTCTCCGGAATTTTCAAGAGATC 632
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Db 1003 AGTGAATTTCTTACTGTCTTCTTCTGTGGAATAGTAATGTACATTACATTGGCATAAT 1062
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Qy 1472 AGGAGCTGTGTGATTTGCTTCTTGTGTTACATAAAGTTTACAAAGATCTGGCCATATCTCACT 1531
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Qy 1712 TTCTGACTCGAGAGTACAACCAATTTGAGGCTTTCAGGCTTCGGAGTCTCGGATCTCTCAC 1771
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Qy 1832 GATGTTTGGGGGGCGGGTTCGTGCTTCTCCCTTGGATCACCACCGGAGCAGAG 1888
Db 1723 GGTGTTCCGGGGGGGAGGTTTCGTGCTTCTGCTGCTTTCGTGCTGCTGAGAGGAG 1779
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## RESULT 2

LOCUS AV109416 3272 bp mRNA linear HTC 25-MAY-2002  
DEFINITION Zea mays CL694.1 mRNA sequence.  
ACCESSION AV109416  
VERSION AV109416.1 GI:21213132  
KEYWORDS HTC.

## SOURCE

ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 3272)

## AUTHORS

Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,  
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.

## TITLE

Maize Mapping Project/DuPont Consensus Sequences for Design of

## JOURNAL

Unpublished (2002)

## REFERENCE

2 (bases 1 to 3272)

## AUTHORS

Coe, E.C.

## TITLE

Direct Submission

## JOURNAL

Submitted (25-APR-2002) Maize Mapping Project, University of



TITLE Rice cDNA from panicle (2000)  
JOURNAL Unpublished (2000)  
COMMENT Contact: Takuji Sasaki  
National Institute of Agrobiological Resources  
Rice Genome Research Program, Kamondai 2-1-2, Tsukuba, Ibaraki  
305-8602 Japan  
Tel: 81-298-38-7441  
Fax: 81-298-38-7468  
Email: tsasaki@abr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/  
PROJECT = 'RGP'.

FEATURES Location/Qualifiers  
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/clone="E31686"  
/clone\_lib="Rice panicle shorter than 3cm"  
/dev\_stage="shorter than 3cm"  
/note="Organ: panicle"  
BASE COUNT 192 a 159 c 172 g 187 t 1 others  
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Query Match 28.2%; Score 656.8; DB 9; Length 711;  
Best Local Similarity 99.4%; Pred. No. 3.8e-128;  
Matches 669; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1648 CTGTCACTCTGAGCTTCATCACCAAGTCCCTGCATTCT-CCTCTCTGCACAGCATG 1706  
Db 1 CTNTCACTCTGAGCTTCATCACCAAGTCCCTGCATTCTCCCTCTCTGCACAGCATG 60  
Qy 1707 CAAGTTCTGACCTCGAGAGTACACCAACATGTGAGCGCTTCAGCTTCGGATGCTC 1766  
Db 61 CAAGTTCTGACCTCGAGAGTACACCAACATGTGAGCGCTTCAGCTTCGGATGCTC 120  
Qy 1767 CTCACCAAGCGACCCACACTGTCACACTACTGCGCAAGTTCGAGCGCGCTGATG 1826  
Db 121 CTCACCAAGCGACCCACACTGTCACACTACTGCGCAAGTTCGAGCGCGCTGATG 180  
Qy 1827 CGACCGATGTTTGGCGGCGGGTTCGTGCCCTTCTCCCTGGATCACCAACCGAGCAG 1886  
Db 181 CGACCGATGTTTGGCGGCGGGTTCGTGCCCTTCTCCCTGGATCACCAACCGAGCAG 240  
Qy 1887 AGCCATGAGGAAGTGAACAGTGAAGAAATGAGATGGAATGGTGTGATGAGGAGAT 1946  
Db 241 AGCCATGAGGAAGTGAACAGTGAAGAAATGAGATGGAATGGTGTGATGAGGAGAT 300  
Qy 1947 ACATGTAATATGTGACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2006  
Db 301 ACATGTAATATGTGACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
Qy 2007 CTGCTAATGAGTGTGTAGTGCCTATATTTCTTCAGAACTTCAGATGGTGCCTCACCA 2066  
Db 361 CTGCTAATGAGTGTGTAGTGCCTATATTTCTTCAGAACTTCAGATGGTGCCTCACCA 420  
Qy 2067 GGCCTAAGAGCAGGAGACCTTCTGATAATGGTTCGGGATGATGGTGTGTGTCAG 2126  
Db 421 GGCCTAAGAGCAGGAGACCTTCTGATAATGGTTCGGGATGATGGTGTGTGTCAG 480  
Qy 2127 GATGAACCTTAGTGTGACACAGGTCATGTGCTCCGACACCTGTAAATTTGTAGAT 2186  
Db 481 GATGAACCTTAGTGTGACACAGGTCATGTGCTCCGACACCTGTAAATTTGTAGAT 540  
Qy 2187 TAACAGCCCCATTTGTACCTGTACCATCTTTAGTTGGCGGGTGTCTTTCCCTAGTTGC 2246  
Db 541 TAACAGCCCCATTTGTACCTGTACCATCTTTAGTTGGCGGGTGTCTTTCCCTAGTTGC 600  
Qy 2247 CACCTGATGTAAATGAATCTCCGCCAAATAGATTTGTGTGTATATAATTTTTC 2306  
Db 601 CACCTGATGTAAATGAATCTCCGCCAAATAGATTTGTGTGTATATAATTTTTC 660  
Qy 2307 TTGGTTGAAAAA 2319  
Db 661 TTGGTTGATAA 673

RESULT 4  
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DEFINITION B312595 Y. Ogihara unpublished cDNA library, wh\_1yf Triticum aestivum cDNA clone wh\_1yf007 5', mRNA sequence.  
ACCESSION B312595  
VERSION B312595.1 GI:20119380  
KEYWORDS EST.  
SOURCE bread wheat.  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.  
REFERENCE 1 (bases 1 to 719)  
AUTHORS Ogihara, Y. and Murai, K.  
TITLE Expressed genes in Triticum aestivum  
JOURNAL Unpublished (2002)  
COMMENT Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp.  
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/tissue\_type="spikelet at early flowering"  
/dev\_stage="Peekes", scale 6"  
/note="Vector: lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; plants were grown under hydroponic conditions at UC Davis, salt stressed for 12 hours, and for 7 days, then dissected and frozen (Akhunov in J Dvorak Lab). Total RNA was prepared from sheath tissue, equal quantities of RNA were pooled from the two samples, polyA was purified from the pooled RNA, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab at the University of California, Riverside (Akhunov, Chin, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 168 a 154 c 178 g 218 t 1 others  
ORIGIN

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Best Local Similarity 87.9%; Pred. No. 5e-109;  
Matches 617; Conservative 0; Mismatches 85; Indels 0; Gaps 0;  
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Db 18 GAGCCCTTTTGTACAGTCTAGTGTTCGGGAGGTTGTGAACGATGCCATCGGT 77  
Qy 869 TGTGCTTTTCAACGACCTACAGAACTTTGATCTTGTCCACATAGATCGGGCTGCTTCT 928  
Db 78 CGTGCTTTTCAACGCGCTCCAGAACTTCGATCTCTAAACAGATCGACGATCGTCAFTCT 137  
Qy 929 GAAATCTTCGGGAACCTCTTTTATTTTTCGTGCGACACCTTCTTGGAGTATTGC 988  
Db 138 TAAGTTCTTCGGGAACCTTCGTACTTATTCGTGTCAGACCTTCTTGGAGTATTGC 197  
Qy 989 TGGATTCCTCAGTGATACATAAATCAAGAGCTATACATTGGAAGGATCTTACTGACCG 1048  
Db 198 TGGATTCCTTAGTGATACGTATCAAGAAATATACATAGGAAGGATCTTACTGACCG 257  
Qy 1049 TGAGTTGCCCTTATGATGCTCATGGCTTACCTTTCATATATGCTGCTGATGTTCTAGA 1108



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Db 258 TGAGTCCCACTTGATGCTCATGGCTACCTCTCATATATGCTAGCTGAGCTGTGAGA 317
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Db 378 TAAAGTACAGAGAGTTCAGAGATTACAAAGACGATTCGCTTTGCAACCTTTGCTTTCAT 437
Qy 1229 TGCTGAGACTTTTCTTCTTCGTATGTGGGATGGATGCAATGGATATTGAATAAGTGGGA 1288
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Qy 1349 TCTGATTTGGAAGAGTCTTTTGTATTTCCCGCTGTCTTCTGTGCAACCTTAACAAGAA 1408
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Qy 1409 GGCACCGAATGAATAAATTAACCTCGAGACGACCAAGTTGTAATATGTTGGCTGGCTGAT 1468
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Db 678 GAGAGGAGCTGTGCTGATCGCTCTTGTCTTACAATAAGTTTAC 719

RESULT 5
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DEFINITION HM000.D12 ITEC HMM Barley Leaf Library Hordeum vulgare cDNA clone
ACCESSION BE420587
VERSION BE420587.1 GI:9418430
KEYWORDS EST.
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases 1 to 1212)
Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier
S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P.,
Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudriet, P.,
Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y.,
Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M.,
Sorrells, M., Warburton, M. and Wenzel, G.
International Triticeae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
Unpublished (2000)
Contact: Herrmann RG
Botanisches Institut der LMU
Menzinger Str. 67, D-80638 Muenchen GERMANY
Fax: 49 30 171683
Email: hermann@botanik.biologie.uni-muenchen.de
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
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/cultivar="Barke"
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/clone="HM000.D12"
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/notes="Vector: bluescripts(-); 850 bp average insert
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296 a 294 c 276 g 346 t

BASE COUNT

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Matches 651; Conservative 0; Mismatches 233; Indels 8; Gaps 3;

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Qy 660 ATATCTCTTTTTCACAAATATCTATGCTGCAATTTGCAATATTCAGCAGAAATGAACATGGA 719
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Qy 780 TGCACATTTGCAGGTCTCAATCAGGATGAGACACCTTTTGTACAGTCTGATTCGGT 839
Db 237 CGCACCTTGCAGGTGTAAAGCCAAAGATGAGACACCTTTTCTGTACAGTTTGTGTGTTGT 296
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Qy 960 TTGTGAGGACCTTCTTGTGAGTATTTGCTGATTTGCTCAGTGCATACATATCAAGAG 1019
Db 417 GCGCGCAGTACCTTTCTTGGAGTATCTAGTGGACTTCTCAGTGTATATGTCATCAAGAAA 476
Qy 1020 CTATACATTTGGAAGGCAATTTCTGACCTGAGTTGCTTATGATGCTCATGGCTTAC 1079
Db 477 CTGTACTTTTGGCAGGCACTTCACTGATCTGAGTGTCTTATGATGCTCATGGCTTAT 536
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RESULT 6
BQ865196
LOCUS
DEFINITION BQ865196
QGC2a03.yg abi QG_ABCDI lettuce salinas Lactuca sativa cDNA clone
QGC2a03, mRNA sequence.
ACCESSION BQ865196

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VERSION      B0865196.1 GI:22250661
KEYWORDS
SOURCE       Lactuca sativa.
ORGANISM     Lactuca sativa.

REFERENCE
1 (bases 1 to 690)
Kozik, A., Micheltmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison
, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)

JOURNAL
COMMENT
Contact: Alexander Kozik [R.W.Micheltmore]
Department of Vegetable Crops, R.W.Micheltmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [micheltmore@vegmail.ucdavis.edu]
Belongs to contig QG_CA Contig6585, see http://cgdb.ucdavis.edu/
for details.
Plate: QGC2 row: a column: 03.
FEATURES
Location/Qualifiers
1..690
/organism="Lactuca sativa"
/cultivar="Salinas"
/db_xref="taxon:4236"
/clone="QGC2a03"
/lab_host="E.coli"
/notice="vector: pBRCNAsfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG LIB=QG ABCDI lettuce salinas
TAG_TISSUE=chemical induction
TAG_SEQ=TTGTAGCGGG"

BASE COUNT  180 a  112 c  149 g  248 t    1 others
ORIGIN
Query Match      17.7%; Score 412.2; DB 14; Length 690;
Best Local Similarity 74.8%; Pred. No. 1.3e-76;
Matches 516; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

Qy 694  GCTGCCATTGCAATTCAGCAGAAATGAACATTTGGAACGCTGGATGTAGGAGATTTCCTT 743
Db 1    GGTGCTATAAATATTTCCAAAGGATGGATGTGGTACCCCTTGAGCTTGGAGACTTTCCTT 60

Qy 744  GCAATTGAGCGCATCTTTCTGGACAGATCTCTGCACATTCGACGTTCTCAATCAG 803
Db 61   GCAATTGAGCAATATTTTCAGCACCCGATTCGGTTTCGACATTTTCGAGGTGTGAATCAG 120

Qy 804  GATGAGACACCCCTTTTGTACAGTCTGGTATTCGGTGAAGTGTGTGTGAACGATGCTACA 863
Db 121  GATCAGACACCTTTATTATATAGTTTGGTGTGGTGAAGTGTGGTGAATGATGCCACA 180

Qy 864  TCAATTGCTTTTCAACGCACTACAGAACTTTGATCTTTGTCACATAGATGCGGCTGTC 923
Db 181  TCAGTTGTCATCTTCAATGCGAGTTCAAAACCTTGATCTCTCTCAAAATCACAACCTGCTGT 240

Qy 924  GTTCTGAATCTTGGGAACTCTTTTATTATTATTTTGTGCGAGCAGCTTCTCTGGAGTA 983
Db 241  GCAATTCAACTGATTGGAAATTTCTTTTATTATTATTCATCAAGACACACTTCTAGGAGCT 300

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Qy 984  TTTGCTGATTGCTCAGTGATACATATCAAGAGCTATATACATTTGGAGGCAATTCCTACT 1043
Db 301  GGAGCTGGGCTACTAAGTGCTTATATATAAGAGCTATATTTTGGAGGCAATTCCTACT 360

Qy 1044  GACCGTAGGTTGGCCCTTATGATGCTCATGCTTACCTTTTCATATATGCTGGCTGAGTTG 1103
Db 361  GATAGAGAAAGTTGCTATAATGATACATAATGATGCTTATCTTTTCATACATGCTAGCTGAGTTA 420

Qy 1104  CTAGATTGTAGCGGCATCTCTCACCGTATCTCTCTGCTGATTTGTAATGTCACATTCACACT 1163
Db 421  TTCTATTGTAGTGGAATCTCTCACCGTATCTCTCTGCTGATTTGTAATGTCACATTCACACT 480

Qy 1164  TGGCAATACGTCACAGAGAGTTCAAGAGTTTACAACAAGACGCGATTTGCAACTCTGTCC 1223
Db 481  TGGCAATATGTCACAGAGAAATCTCGAGTAATACTACCAAGCATACCTTTGCAACATTTGTCA 540

Qy 1224  TTCAATTGCTGAGACTTTTCTCTCTGATGTTGGGATGGATGGATGATGATTTGAAAAA 1283
Db 541  TTTGCTGCTGAGTTTATTTATCTTTCTTTATGTCGAAATGGATGCTCTCATTCACACT 600

Qy 1284  TGGGAGTTTGGCCAGTGACAGACCTGGCAATTCATTTGGGATAAGCTCAATTTTGTCTAGGA 1343
Db 601  TGGAGAGTTTGTAAAGACAGCCCTGGGACTTCNGTTGAAGTGGTGCATTTTATTTGGGA 660

Qy 1344  TTGCTTCTGATTGGAAGAGCTGCTTTTGTGA 1373
Db 661  TTGCTTTTAGTTGGAAGAGAGCCCTTTGTGA 690

RESULT 7
LOCUS     BI933988                665 bp    mRNA    linear    EST 18-OCT-2001
DEFINITION EST553877 tomato flower, anthesis Lycopersicon esculentum cDNA
clone CTOD18B13 5' end, mRNA sequence.
ACCESSION BI933988
VERSION    BI933988.1 GI:16248460
KEYWORDS  EST.
SOURCE     tomato.
ORGANISM   Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE  1 (bases 1 to 665)
AUTHORS   Van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J.,
Unterback, T., Van Aken, S., Ronning, C.M., Niemman, W., Fraser, C.M.,
Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from tomato flower tissue, anthesis (2001)
Unpublished (2001)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3
Location/Qualifiers
1..665
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cTOD18B13"
/clone_lib="tomato flower, anthesis"
/tissue_type="flower"
/dev_stage="anthesis"
XhoI; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
BASE COUNT  156 a  140 c  144 g  225 t

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## ORIGIN

Query Match 17.2%; Score 400.6; DB 13; Length 665;  
Best Local Similarity 75.3%; Pred. No. 3.5e-74;  
Matches 499; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

Qy 746 AATTGGAGCCATCTTTCTGCGACAGATTCTGTCTGCACATTCGAGTCTCTCAATCAGGA 805  
Db 1 AATTGGAGCAATATTGCTGCCACAGATTCTGTCTGCACATTCGAGTCTCTCAATCAGGA 60  
Qy 806 TGACACACCCCTTTTGTACAGTCTGGTATTCGGTGAAGGTGTTGTGACGATGCTACATC 865  
Db 61 TGACACACCCCTCTTTTACAGTCTGTATTTGGAGAGAGATTGTGAATGATGCTACATC 120  
Qy 866 AATTGTGCTTTTCAACGCACATACAGAACTTTGATCTTGTCCACATACATCGCGCTGTGCT 925  
Db 121 GGTGGTCTTTTCAATGCTATTCAAAAGTTGACCTTACAGCTTGAATCCAGTATAGC 180  
Qy 926 TCTGAATTTCTTGGGAACTTCTTTTATTTATTTTGTGAGCACCCTTCTTGGAGTATT 985  
Db 181 CCTCAGTTTCTTGGCAACTTCTTCTATCTGTTCTTGTAGCACTTTTACTGGAGCAGG 240  
Qy 986 TGTGATGCTCAGTCATACATAAATCAAGAACATATATCGGAAGGCAATCTACTGA 1045  
Db 241 AACTGGTCTTCTTAGTGTCTTACATTATCAAGAAGCTGTATTTTGGCAGGCACTCCAGA 300  
Qy 1046 CCGTGAGGTTGCCCTTATGATGCTCATGGCTTACCTTTTCATATATGCTGCTGAGTTGCT 1105  
Db 301 TCGTGAGGTTGCCCTTATGATGCTCATGGCTTATTTATCATACATGCTGCCGAATATT 360  
Qy 1106 AGATTGAGCGGCAATCTCACCGTATTCTTCTGTGGTATTGTATGTCACTATACACTTG 1165  
Db 361 CTATTTGAGTGGATTCTCACCGTATTCTTCTGTGGTATTGTATGTCTCATTACACTTG 420  
Qy 1166 GCATACTGTCAGAGAGTCAAGAGTTCAAGAGTTCAACAAAGCAGCATTTGCCAATCTGTCTT 1225  
Db 421 GCACAAATGTGACCGAGAGTCAAGAGTCACTTCAAGGACACACTTTTGCAACTTTGTCAAT 480  
Qy 1226 CATTGCTGAGACTTTCTCTTCTGTATGTTGGATGGATGATGATGATGATGATGATGATG 1285  
Db 481 TCTTGCAGAGACTTTCTCTTCTGTATGTTGGATGGATGATGATGATGATGATGATGATG 540  
Qy 1286 GGAGTTTCCAGTGCAGACCTGGCAATCAATTCATGGATAGCTCAATTTTGTAGGATT 1345  
Db 541 GAAATTTGTTGTGACAGGCTGGATATCAATTTCCGCAAGTTCGATCTGATGGGACT 600  
Qy 1346 GGTCTGATTTGGAAGAGTCTTTTGTATTCCTGCTGTGTTTGTGTCGAACCTTAACAA 1405  
Db 601 AATCTTGTGGGAGACCTGCTTTTGTGTTTTCATATCATCTATATCACTTATCAATGAA 660  
Qy 1406 GAA 1408  
Db 661 GAA 663

RESULT 8  
BJ316128  
LOCUS BJ316128 632 bp mRNA linear EST 09-APR-2002  
DEFINITION BJ316128 Y. Ogiwara unpublished cDNA library, Wh\_yf Triticum  
aestivum cDNA clone whyf21k06 5', mRNA sequence.

ACCESSION  
VERSION BJ316128  
BJ316128.1 GI:20121504

KEYWORDS  
EST.

SOURCE  
bread wheat.

ORGANISM  
Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae  
; Triticeae; Triticum.

1 (bases 1 to 632)

Ogiwara, Y. and Murai, K.

Expressed genes in Triticum aestivum

JOURNAL  
Unpublished (2002)

CONTACT: Tadasu Shin-i

## Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

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Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

Location/Qualifiers

## FEATURES

source

1. 632

/organism="Triticum aestivum"

/cultivar="Chinese Spring"

/db\_xref="taxon:4565"

/clone="whyf21k06"

/tissue\_type="spikelet at early flowering"

/dev\_stage="Feekes' scale 6"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid;

Site 1: EcoRI; Site 2: XhoI; Plants were grown under

hydroponic conditions at UC Davis, salt stressed for 12

hours, and for 7 days, then dissected and frozen (Akhunov

in J Dvorak Lab). Total RNA was prepared from sheath

tissue, equal quantities of RNA were pooled from the two

samples, polyA was purified from the pooled RNA, a cDNA

library was made, and the cDNA clones were in vivo

excised to give plasmid clones in the TJ Close lab

at the University of California, Riverside (Akhunov, Chin

, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).

Plasmid DNA preparations and DNA sequencing were

performed in the OD Anderson lab (all other authors)."

## BASE COUNT

146 a 196 c 134 t

## ORIGIN

Query Match

Best Local Similarity 17.0%; Score 396; DB 13; Length 632;

Matches 456; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 1362 GTGCTTTTGTATTCGCGTCTGTTCTTGTGCGAATCTTCAAGAGGACCGAATGAA 1421

Db 1 GCTGCTTTGCTTCCGCTCTGTTCTTATCCAACTCTGACAAAGAGCGAGCTTGA 60

Qy 1422 AAAATAAAGCTGAGACAGCAAGTCTAATATGCTGGCTGGCTGATGAGAGAGCTGTG 1481

Db 61 AAAATAAAGCTGAGAGAGCAATCTAATATGCTGGCTGGCTGATGAGAGAGCTGTG 120

Qy 1482 TCGATTGCTTTGCTTTACAAATAGTTTACAAGATCTGGCCATCTCAGCTGACGGCAAT 1541

Db 121 TCGATGCTTTGCTTTACAAATAGTTTACAAGATCTGGCCATCTCAGCTGACGGCAAT 180

Qy 1542 GCAATAATGATCACCAGACCAATCACTGTCTGTTCTTTTAGCACTATGTTATTTGGGATG 1601

Db 181 GCGATAATGATCACCAGACCAATCACTGTCTGTTCTTTTAGCACTATGTTATTTGGGATG 240

Qy 1602 ATGACAAAGCCATTGATCAGGCTGTCTACCGCTCTCAGGCTCTCTGTCTACCTCTGAG 1661

Db 241 TTGACAAAGCCCTGATCCGGTCTCTGCTGCGCGGTGAGCAAGCGGCCCTCGGAC 300

Qy 1662 CTTTCATACCAAGTCCCTGCAATCTCTCTCTTCAAGCATGCAAGTCTTCTGACCTC 1721

Db 301 CCGCGTCTACCGAGTCTCTGCACTCTCTCTCTCTCAAGCCAGCTAGGCTCGGACCTG 360

Qy 1722 GAGAGTACCAACCAATTTGTAGGCTTCCAGCTCTCGGATGCTCTTACCAAGCGGAC 1781

Db 361 GAGGCGCTCTCTCCATCTGAGGCTCTCAGCTCTCGGATGCTCTATCAACCAAGCGGAC 420

Qy 1782 CACACTGTCCACTTACTTCTGGCGAGTTCGACGCGCTGATGGACCGATGTTTGGC 1841

Db 421 CACACATCCACTTACTTCTGGCGAGTTCGACGCGCTGATGGCGCGATGTTTGGT 480

Qy 1842 GGGCGGGTTCGTGGCTTCTCCCTGATCAACCAAGCAGAGCATCGGAGGAGAA 1901

Db 481 GGGCGGGTTCGTGGCTTCTCCCTGATCAACCAAGCAGAGCATCGGAGGAGAA 540

Qy 1902 TGAACAGTCAAGAA 1917

Db 541 TGAACGTCGCGAAGAA 556

# RESULT 9

BQ512490

LOCUS

DEFINITION

Accession

Version

Keywords

Source

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

Source

Location/Qualifiers

1. .802

/organism="Solanum tuberosum"

/cultivar="Kennebec or Binjete"

/db\_xref="taxon:4113"

/clone="STMHY71"

/microarray analyses mixed potato tissues"

/tissue type="mixed tissues"

/lab host="SOLR"

/note="vector: plusescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Combination of untreated and Phytoththora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes

of tubers, or roots."

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

559; Conservative

0; Mismatches

233; Indels

9; Gaps

2;

Qy 1084

Db 2

Qy 1144

Db 62

Qy 1204

Db 122

Qy 1264

Db 182

Qy 1324

Db 242

Qy 1384

Db 302

Qy 1444

Db 362

Qy 1504

Db 422

Qy 1564

Db 482

Qy 1624

Db 542

Qy 1678

Db 602

Qy 1735

Db 662

Qy 1795

Db 722

Qy 1855

Db 782

RESULT 10

LOCUS

DEFINITION

Accession

Version

Keywords

Source

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

Source

Location/Qualifiers

1. .733

/organism="Lactuca sativa"

Plate: QGG5

row: E

column: 06.

Location/Qualifiers

1. .733

/organism="Lactuca sativa"

Unpublished (2002)

Contact: Alexander Kozik [R.W.Michelmoe]

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Amundson Hall UCD, Davis, CA 95616, USA

Tel: 1-(530)-742-1742

Fax: 1-(530)-752-9659

Email: akozik@ucdavis.edu

belongs to contig QG\_CA\_Contig6585, see http://cgdb.ucdavis.edu/

for details.

Letuce and Sunflower ESTs from the Compositae Genome Project

http://compositae.ucdavis.edu/

Unpublished (2002)

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for details.

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http://compositae.ucdavis.edu/

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Unpublished (2002)

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for details.

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for details.

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http://compositae.ucdavis.edu/

Unpublished (2002)

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Tel: 1-(530)-742-1742

Fax: 1-(530)-752-9659

```

/cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="OG5806"
/clone_lib="OG_EFGHJ lettuce serriola"
/lab_host="E.Coli"
/notes="vector: pBRCDNA5fiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpb.ucdavis.edu/
TAG LIB=OG_EFGHJ lettuce serriola
TAG_TISSUE=flowers environmental stress
TAG_SEQ=CGAATCGCGG"
BASE COUNT 175 a 134 c 146 g 278 t
ORIGIN

Query Match 15.7%; Score 366.6; DB 14; Length 733;
Best Local Similarity 70.9%; Pred. No. 5e-67;
Matches 486; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

Qy 340 CGACTCGACTACGCGTGGTGTCCTCAACCTGTCGTCGCGCTGTCGCGCT 399
Db 47 CTAGCTCTGAGTACTCTTCCATTGCTCTATGAACCTGTTGTTGCTCTTCTTTGTCCT 106
Qy 400 GCATCGCTCCGCGCACCTCTCCAGAGAGATCGCTGGTCAATGAGTCCATCACCGCGC 459
Db 107 GTATCGTAATCGGTCACTCTTTGGAAGAGATCGATGATGAACGAATCATCACTGCC 166
Qy 460 TCATCATCGGCTCTGCACCGCGTGGTGATCTTGCTGATGACCAAGGAAAGAGTCCGC 519
Db 167 TTGTCATGGTATTGCACTGGAGTGTATTGTTGTAAGCAGTGGAGAACAAATTCAC 226
Qy 520 ACTTATGCTCTCAGTGAGAGATCTTCTTCACTACCTACCTCCCTCCGATCATCTTCA 579
Db 227 ATCTTCTAGCTTCAGTGAAGATCTTCTTCAATTTATCTTCTCCACCTATCATCTTCA 286
Qy 580 ATGAGGTTTTCAGTTAAGAAAGCAATCTTCCGGAATTTTCATGACCATCATATAT 639
Db 287 ATGCTGGGTTTCAGTTAAGAAAGCAATTTTTCGCAATTTTCATGACCATTTGCTAT 346
Qy 640 TTGAGCGCTCGGACAAATGATATCTTTTTCACAAATATCTATTGCTGCCATTCGAATAT 699
Db 347 TTGGTGCTTTGGCACTGTGATATCTTTCACCATCATATCATTTGGTGCTATAAATTT 406
Qy 700 TCAGCAGAAATGAACATTTGGAACGCTGGAGATGTTTCTTTCGCAATTTGGAGCCATCT 759
Db 407 TCCAAAGGATGGATGTTGGTACCTTGGAGCTTGGAGACTTCTTTCGCAATTTGGTCAATAT 466
Qy 760 TTTCTGCGACAGATCTGCTGCAATTCGAGCTTCCATGAGTGCATGAGACACCTTTT 819
Db 467 TTTGAGCACCAGATTCGGTTTGGCACTTTGCAAGGTGTTGAATCAGGATCAGACACCTTAT 526
Qy 820 TGTACAGTCTGGTATTCGGTGAAGGTGTTGTAACGATGCTTACATCAATTTGCTTTTCA 879
Db 527 TATATAGTTTGGTTGGTGAAGGTGTTGTAATGATGACCATCATGTTGTCATCTTCA 586
Qy 880 ACGCACTACAGAACTTTGATCTTGTCCATAGATGCGGCTGTCGTTCTGAAATTTCTGG 939
Db 587 ATGCAAGTTCAAACTTTGATCTCTCTCAATCACAATCGCTGTTGCAATTCACATGATTG 646
Qy 940 GGAAGTCTTTTATTTATTTTGTGCGAGCACCTTCTTGGAGTATTTGCTGGATGCTCA 999
Db 647 GAAATTTCTTTTATTTATTCATCAACAGCACACTTCTTAGGAGCTGGAGCTGGGCTACTAA 706
Qy 1000 GTGCATACATAATCAAGAAGCTATA 1024
Db 707 GTGCTTATATTATAAGAGCTATA 731

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# RESULT 11 BQ612167 LOCUS

DEFINITION BQ612167 607 bp mRNA linear EST 26-JUN-2002  
sap80d01.v1 Gm-cl087 Glycine max cDNA clone SOYBEAN CLONE ID:  
Gm-cl087-7057 5', similar to TR:Q9SS27 Q9SS27 PUTATIVE SODIUM PROTON  
EXCHANGER. ; mRNA sequence.

## ACCESSION BQ612167 VERSION BQ612167.1 GI:21601836 KEYWORDS EST. SOURCE soybean. ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

## REFERENCE 1 (bases 1 to 607) AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelidng,J., Corvett,V., Khanna

,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,  
Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,  
R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann  
R., Waterston,R. and Wilson,R.  
Public Soybean EST Project

## Unpublished (1999) TITLE Public Soybean EST Project JOURNAL Contact: Shoemaker R/Public Soybean EST Project COMMENT Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130  
South Memorial Parkway Huntsville, AL 35801 For further information  
call: (800)-533-4363 or contact: cu@resgen.com web site:  
www.resgen.com

Seq primer: -40RP from Gibco  
High quality sequence stop: 479.  
Location/Qualifiers  
1..607

## FEATURES source

/organism="Glycine max"  
/db\_xref="taxon:3847"  
/clone="SOYBEAN CLONE ID: Gm-cl087-7057"  
/clone\_lib="Gm-cl087"  
/tissue\_type="Roots"  
/lab\_host="DH10B"  
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:  
XhoI. The mRNA was prepared using polyattract mRNA system  
from PROMEGA. The cDNA was prepared using the STRATAGENE  
kit. Complementary DNA was synthesized from mRNA using a  
primer consisting of a poly(dT) sequence with a XhoI  
restriction site  
(5'GAGAGAGAGAGAGAGAACTAGTCTCGAGTTTTTTTTTTTTTTTTTTT).

EcoRI adapters (5'-OH-AATTCGACGAG and 3'-GCGTGTCTCp) were  
ligated to the blunt-ended cDNA fragments followed by XhoI  
digestion. The cDNA fragments were directionally cloned  
into the EcoRI-XhoI restriction sites of the pBluescript  
vector. The vector was previously dephosphorylated. The  
ligated cDNA fragments were transformed into DH10B by  
electroporation. Library is in LB medium with ampicillin  
and glycerol 8%. Average insert size: 800 bp."

BASE COUNT 141 a 118 c 133 g 215 t

## ORIGIN

Query Match 15.6%; Score 362.8; DB 14; Length 607;  
Best Local Similarity 76.5%; Pred. No. 3.4e-66;  
Matches 445; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

Qy 803 GGATGAGACACCTTTTGTACAGTCTGGTATTCGGTGAAGGTGTTGGAACGATCTAC 862  
Db 25 GGATGAGACACCTTTGCTGACAGTCTTGTATTTGGGAGGGTGTGTGAATGATCTAC 84  
Qy 863 ATCAATTTGCTTTTCAACGCACTACAGAACTTTGATCTTGTCCATAGATGCGGCTGT 922

Db 85 ATCAGTGGTCTTTTCAATGCAATCAAAAGCTTTGACCTCAACCAAAATGACTCTTCAAT 144

Qy 923 CGTCTGAAATCTTGGGAACTCTTTTATTTATTTTGTGAGCAGCACTCTCTTGGAGT 982

Db 145 TGCTGTACATTTTGGGAAATTTCTGTATCTATTTATGCAAGCAACATGCTTGGAGT 204

Qy 983 ATTTCTGGAATTCAGTGCATACATATCAAGAGCTATACATTTGGAAGCAATCTTAC 1042

Db 205 TTTGACAGGTCTACTAGTGTCTTACATTTAAAAAGCTGTACATTTGGCAGGCACTCTAC 264

Qy 1043 TGACGTGAGTTGCCCTTATGATGCTCATGCTTACCTTTTCATATATGCTGGCTGAGTT 1102

Db 265 AGATCGTGAAGTTGCTCTATGATGTATATGATGATGATGATGATGATGATGATGAT 324

Qy 1103 GCTAGATTGACGGCATCTCACCGTATTCTTCTGTGTATTTGTAATGTCATATTACAC 1162

Db 325 ATGTTATCTGAGTGCATCTCACGTATCTTTTGTGTATTTGTAATGTCATATTACAC 384

Qy 1163 TTGGCAATACGTCACAGAGAGTTCAAGAGTTACAAAGCAAGCAAGCAATTTGCAACTCTGTC 1222

Db 385 CTGGCAATACGTCACAGAGAGTTCAAGAGTTCAAGAGTTCAAGAGTTCAAGAGTTCAAG 444

Qy 1223 CTTCAATGCTGAGATTTCTCTCTGTATGTTGGATGATGATGATGATGATGATGATGAT 1282

Db 445 ATTTGTTGCTGAGATCTTTATCTCTCTTTATGTTGGATGATGATGATGATGATGATGAT 504

Qy 1283 ATGGAGTTTGGCAGTGACAGACCTGGCAATCCATTTGGATGATGATGATGATGATGATGAT 1342

Db 505 ATGGAATTCGTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 564

Qy 1343 ATTTGTTCTGATTTGAAGAGTGTCTTTTGTATTTCCCGCTGTC 1384

Db 565 TCTAATCTCTTGGAGAGCAGCTTTTGTGTTTCCCGCTATC 606

RESULT 12

BQ163913 666 bp mRNA linear EST 24-APR-2002

LOCUS 952081B08.x1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea

DEFINITION mays cDNA, mRNA sequence.

ACCESSION BQ163913

VERSION BQ163913.1 GI:20300970

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 666)

Walbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford University

Unpublished (1999)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 952081 row: B column: 08.

Location/Qualifiers

1. .666

/organism="Zea mays"

/cultivar="BMS (Black Mexican Sweet)"

/db\_xref="taxon:4577"

/clone\_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"

/tissue\_type="suspension culture"

/dev\_stage="mixed logarithmic and stationary growth phases"

/lab\_host="DH10B"

/note="Vector: pUC19; Site\_1: EcoRI; Site\_2: EcoRI; The

library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

BASE COUNT 149 a 155 c 153 g 209 t

ORIGIN

Query Match 15.5%; Score 361; DB 14; Length 666;

Best Local Similarity 71.4%; Pred. No. 7.8e-66;

Matches 475; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

Qy 444 GAGTCCATCAGCGGCTCATCGGGCTCTGCACCGCGTGGTGAATCTTCTGTAAGACC 503

Db 2 GAGTCCATCAGCGGCTCTTTCATCGGGCTGGAACTGGAGCGGTCTCTCTGTCGCTCG 61

Qy 504 AAAGGAGAGCTCGCACTTATTCGTCTTCAAGTGAAGATCTCTTCTTCTCATCTCTCTC 563

Db 62 AGCGGGAAGCAATTCGCGGCTGCTGTTTACGAGGACCTCTCTTATTTACCTGCTG 121

Qy 564 CTTCCGATCATCTTCAATGCAAGTCTTTCAGGTAAGAAAAAGCAATCTTCCGGAATTC 623

Db 122 CGCGGATCATATTCAATGCAAGGTTCCAACTGAAGAAGAACAGTCTTTTGGAACTTC 181

Qy 624 ATGAGATCAATTTATTTGGAGCGCTGGGACAATGATATCTTTTTCACAAATATCTATT 683

Db 182 ATTACTATTACATGTTTGTGTGCACTTGGCACTTGTATCTCTTTTACTGTAAATATCCCTT 241

Qy 684 GCTCCATTGCAATATTTCAGCAGAAATGAACATTGCAACGCTGGATGTAGGAGATTTCTT 743

Db 242 GCGCTCTAGACTTAATTAAGGCTTAATTCGCGCACTTGAACCTGGAGACTATCTT 301

Qy 744 GCAATTGGAGCCATCTTTTCTGCGACAGATTTCTGTCTGCACATTTGCAAGTCTCTCAATCAG 803

Db 302 GCACCTTGGGGCAATATTCTCGGCCACAGACTCGGTTTGCACCTTGCAGGTGTAAAGCAA 361

Qy 804 GATGAGACACCTTTTGTACAGTCTGGTATTCGGTGAAGTGTGTGAAGCATGCTACA 863

Db 362 GATGAGACACCAATCTTTGTACAGCTCTGTGTTGTGTAAGGTTGTGCAATGACGCAACT 421

Qy 864 TCAATTGTCCTTTTCAAGCACTACAGAACTTTTCATCTTGTCCACATAGATGCGGCTGTC 923

Db 422 TCTGTTGTTGTTTCAATGCAATCCAGAACTTTGATCTCTGGAAATATCAGCAGTGCCAAA 481

Qy 924 GTTCTGAAATTTCTGGGGAACCTCTTTTATTTATTTTGTCTGAGCACCCTTCTCTTGGAGTA 983

Db 482 TTAAGTAACTTCAATGGCAGTTTCTTTATCTGTTCTGCTCCAGCACCATTCTTGGAGTA 541

Qy 984 TTTGCTGATTTGCTCAGTGCATATCAATTAAGAAGCTATACATTTGGAAGCATTTCTACT 1043

Db 542 GCTTCTGAGCTTCTTAGTGTCTTATACCAATTAAGAAGTTGTATCTCGGCAAGCATTTCAACC 601

Qy 1044 GACCGTGAGTTGCCCTTATGATGCTCATGCTTACCTTTTCATATATGCTGCTGAGTTG 1103

Db 602 GATCGTAAGTTTCCATTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 661

Qy 1104 CTAGA 1108

Db 662 CTCGA 666

RESULT 13

LOCUS BQ317459

DEFINITION BQ317459 Y. Ogihara unpublished cDNA library, wh\_yf Triticum aestivum cDNA clone whyf28e02 5', mRNA sequence.

ACCESSION BQ317459

VERSION BQ317459.1 GI:20122274

KEYWORDS EST.



SOURCE  
ORGANISM  
bread wheat.  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae  
; Triticeae; Triticum.  
REFERENCE  
AUTHORS  
Ogihara, Y. and Murai, K.  
TITLE  
Expressed genes in Triticum aestivum  
JOURNAL  
Unpublished (2002)  
COMMENT  
Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@gene.nig.ac.jp.  
FEATURES  
source  
location/Qualifiers  
1..638  
/organism="Triticum aestivum"  
/cultivar="Chinese Spring"  
/db\_xref="taxon:4565"  
/clone="whyf28e02"  
/clone\_lib="V. Ogihara unpublished cDNA library, Wh\_yf"  
/tissue\_type="spikelet at early flowering"  
/dev\_stage="Feekes' scale 6"  
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;  
Site 1: EcoRI; Site 2: XhoI; Plants were grown under  
hydroponic conditions at UC Davis, salt stressed for 12  
hours, and for 7 days, then dissected and frozen (Akhunov  
in J Dvorak lab). Total RNA was prepared from sheath  
tissue, equal quantities of RNA were pooled from the two  
samples, polyA was purified from the pooled RNA, a cDNA  
library was made, and the cDNA clones were in vivo  
excised to give pBluescript phagemids in the TJ Close lab  
at the University of California, Riverside (Akhunov, Chin  
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).  
Plasmid DNA preparations and DNA sequencing were  
performed in the OD Anderson lab (all other authors)."  
BASE COUNT 115 a 185 c 178 g 160 t  
ORIGIN  
source  
Query Match 15.4%; Score 359.4; DB 13; Length 638;  
Best Local Similarity 75.9%; Pred. No. 1.7e-65;  
Matches 444; Conservative 0; Mismatches 141; Indels 0; Gaps 0;  
Qy 181 CATTCACCAACGAGGAGGAGTGGATTGGTTTAAAGCTCCGCACTTGGCGG 240  
Db 54 CGTTTCGGATTAGCAAGGGCGGCTCGAGCTGGGTTGATTGTATCCAAAGCTCGCGTAT 113  
Qy 241 GAAATCTCGCTCTCTCTCGGTGGGTGGCGGAGAGTCCGCGCGGTGAGGCATGG 300  
Db 114 TTCCCGGGAATCTTCTCTCTGACGAGGAGGAGCGGCGGGGATGGGTACCAAG 173  
Qy 301 GGATGGAGGTGGCGGCGGCTGGGGGTCTGTGACACGACTTCGACTACGGCTCGG 360  
Db 174 TGGTGGCGCGAGCTGGCGGCTGAGCGGCGGCTGGGCACTTCGGACCAACGCTCCG 233  
Qy 361 TGGTCTCCATCAACCTGTCTCGCGGCTGCTCGGCTGATCGTCTCGGCCACCTCC 420  
Db 234 TGGTCTCCATCAACCTGTCTCGCGGCTGCTCGGCTGATCGTCTCGGCCACCTCGC 293  
Qy 421 TCGAGGAGATCGCTGGGTCAATAGTCCATCACC CGGCTCATCATCGGGCTCTGCACCG 480  
Db 294 TCGAGGAGNACGCTGGCTCAACAGATCCATCACC CGCCTCATCATCGGGCTGTGCACG 353  
Qy 481 GCGTGGTATCTGTGATGACCAAGGGAAGAGCTCGCACTTATTCGCTTCAGTGAGG 540  
Db 354 GCGTGGTATCTGTGATGACCAAGGGAAGAGCTCGCACTGCTGCTCTTCAGCGAGG 413  
Qy 541 ATCTCTTCTTACCTCTCCCTCCGATCATCTTCAATGCAGGTTTTCAGGTAAAGA 600  
Db 414 ACCTCTTCTTACCTCTCCCTCCGATCATCTTCAAGCGCGGTTTCCAGGTGAAGA 473

Qy 601 AAAAGCAATCTTCCGGAATTTTCATGACGATCACATTAATTTGGAGCCGTCGGACAATGA 660  
Db 474 AGAAGCAGTCTTCCGGAATTTTCATGACAAATCACACTATTTGGTCGCGTGGGACGATGA 533  
Qy 661 TATCCTTTTTCACAATATCTATTGCTGCCATTCGCAATATTCAGCAGAAATGAACATTGGAA 720  
Db 534 TGTGCTTTTTCACAATATCTCTGCTGCCATTCGCAATATTCAGCAGGATGAACATTGGGA 593  
Qy 721 CGCTGATGTAGGAGATTTTCTTTCGAATTTGGAGCCATCTTTTCTG 765  
Db 594 CACTGGATGTATCAGATTTTCTTTCGAATTTGGAGCTATCTTTCCG 638  
RESULT 14  
BM109451  
LOCUS  
DEFINITION  
EST556987 potato roots Solanum tuberosum cDNA clone cPRO4A24 5' end  
BM109451  
VERSION  
BM109451.1 GI:17070373  
KEYWORDS  
EST.  
SOURCE  
potato.  
ORGANISM  
Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
REFERENCE  
AUTHORS  
van der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Aken, S.,  
Utterback, T., Chiemiango, A., Bougri, O., Buell, C.R., Ronning, C.,  
Tanksley, S. and Baker, B.  
TITLE  
Generation of ESTs from potato roots  
JOURNAL  
Unpublished (2001)  
COMMENT  
Contact: Research Genetics, Libraries Division  
Tel: 1-800-711-6195  
Email: cdna@resgen.com  
For clone info: please contact Research Genetics, Libraries  
Division tel 1-800-711-6195, email cdna@resgen.com  
Seq primer: r3.  
FEATURES  
Location/Qualifiers  
1..637  
/organism="Solanum tuberosum"  
/cultivar="Kennebec"  
/db\_xref="taxon:4113"  
/clone="cPRO4A24"  
/clone\_lib="potato roots"  
/tissue\_type="roots"  
/dev\_stage="in vitro grown stem cuttings"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:  
XhoI; supplier: Cornell University, Tanksley lab;  
sequencing: The Institute for Genomic Research. Roots were  
isolated from in vitro grown stem cuttings on CM medium.  
Roots were isolated two weeks after placing the stem  
cuttings from in vitro grown plants on medium."  
BASE COUNT 170 a 135 c 142 g 190 t  
ORIGIN  
source  
Query Match 14.7%; Score 343.6; DB 13; Length 637;  
Best Local Similarity 76.5%; Pred. No. 3.7e-62;  
Matches 421; Conservative 0; Mismatches 129; Indels 0; Gaps 0;  
Qy 1084 CATATATGCTGGCTGAGTTGCTAGATTGGAGCGCAATTCACCGTATTTCTTCTGTGGTA 1143  
Db 2 CATACATGCTGGCTGAATCTTCTTGTAGTGGGATTCCTACTGTATTTTCTGTGGTA 61  
Qy 1144 TTGTATGTCAATACATCTGGCATACGTCACAGAGTTCAAGAGTTACACAAAGC 1203  
Db 62 TTGTAAATGTCTATTACATCTGGCAATGTGACCGAGAGTTCAAGAGTCACTACAAGGC 121  
Qy 1204 ACCGATTTGCAACTGTCTCTTCATTCGCTGAGACTTTTCTTCTCCGTATGTTGGATGG 1263  
Db 122 ACGCTTTTGCACCTTGTGTCAATTTCTTTCGAGAGACTTTCCTCTTCTCTATGTGCGGATGG 181





QY 1264 ATGCATTGGATATGAAAAATGGAGTTTCCAGTGACAGACCTGGCAATCCATTGGGA 1323  
 Db 182 ATGCTTTGGATATCGAAGCTGGAATTTTGTGTCAGAGGCTGGATTATCAATTTCCG 241  
 QY 1324 TAAGCTCAATTTTGTAGGATTTGGTCTGATGGAGAGAGCTGTTTGTATTTCCGCTGT 1383  
 Db 242 TGAGTTCAATTAAGTGGGATTAATCTGTCTGGGGAGAGCTGCTTTGTTTTCATTAT 301  
 QY 1384 CGTTCTTGTGCAACCTTAACAAAGGACCCGAATGAAAAATAAACCCTGGAGACAGCAAG 1443  
 Db 302 CATCTCTCAACTTAATGAGAAATCTCGGAGCAAAAAATATCACTTTAGGACAGCAAG 361  
 QY 1444 TTGTAATATGGTGGCTGGCTGATGAGAGAGCTGTGTGATTTGCTTTGCTTTACAATA 1503  
 Db 362 TGATAATATGGTGGCAGGTTTGTATGAGAGGCGCAGTGTCCATGGCACTGGCATATAA 421  
 QY 1504 AGTTTACAGATCTGGCCATCTAGCTGACAGGCAATGCAATGATATGATCAGACCA 1563  
 Db 422 AGTTTCACTCGTGGGGACACACTCAACTGCAGGACAATGCAATGATATGATCAGACCA 481  
 QY 1564 TCACTGTGCTTTCTTTTAGCACTATGATTTTGGGATGATGACAAAGCCATTGATCAGGC 1623  
 Db 482 TRACCAATGTTCTATTTCAGCACAAATGATTCGTTTATGACAAAAACCCCTTATAAGTC 541  
 QY 1624 TGCTGTAC 1633  
 Db 542 TCCTGTGCC 551

## RESULT 15

C91832 378 bp mRNA linear EST 04-APR-2002  
 LOCUS C91832 Rice panicle shorter than 3cm Oryza sativa (japonica  
 DEFINITION cultivar-group) cDNA clone E31686\_1A, mRNA sequence.  
 ACCESSION C91832  
 VERSION C91832.1 GI:3061200  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group).  
 ORGANISM Oryza sativa (japonica cultivar-group).  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.  
 1 (bases 1 to 378)  
 Sasaki, T. and Yamamoto, K.  
 Rice cDNA from panicle  
 Unpublished (1997)  
 JOURNAL  
 COMMENT Contact: Takuji Sasaki  
 National Institute of Agrobiological Resources  
 Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki  
 305-8602, Japan  
 Tel: 81-298-38-7441  
 Fax: 81-298-38-7468  
 Email: tsasaki@abr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/  
 PROJECT = 'RGP'  
 POLYA=No.

## FEATURES

source Location/Qualifiers  
 1..378  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /cultivar="Nipponbare"  
 /db\_xref="taxon:39947"  
 /clone="E31686\_1A"  
 /clone\_lib="Rice panicle shorter than 3cm"  
 /dev\_stage="shorter than 3cm"  
 /note="Organ: panicle"  
 BASE COUNT 88 a 74 c 89 g 121 t 6 others  
 ORIGIN

Query Match 14.6%; Score 340.4; DB 14; Length 378;  
 Best Local Similarity 95.0%; Pred. No. 2.1e-61;  
 Matches 359; Conservative 0; Mismatches 17; Indels 2; Gaps 1;  
 QY 1013 CAAGAAGCTATACATTGGAGGCAATCTACTGACCGTAGGTTGGCCTTATGATGCTCAT 1072  
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Db 1 CAAGAAGCTATACATTGGAGGCAATCTACTGACCGTAGGTTGCCCTTATGATGCTCAT 60  
 QY 1073 GGCTTACCTTTTCATATATGCTGGCTGAGTTGCTAGATTGAGCGGCATTTCTCACCGTATT 1132  
 Db 61 GGCTTACCTTTTCATATATGCTGGCTGAGTTGCTAGATTGAGCGGCATTTCTCACCGTATT 120  
 QY 1133 CTTCTGTGGTATTGTAATGTACATTACACTTGGCATAAGCTCAGAGAGTTTCAAGAGT 1192  
 Db 121 CTTCTGTGGTATTGTAATGTACATTACACTTGGCATAAGCTCAGAGAGTTTCAAGAGT 180  
 QY 1193 TACAACAAAGCAGCAATTTGCAACTCTGTCTCTTCATTGCTGAGACTTTTCTTCTCTGTA 1252  
 Db 181 TACAACAAAGCAGCAATTTGCAACTCTGTCTCTTCATTGCTGAGACTTTTCTTCTCTGTA 240  
 QY 1253 TGTGGGATGGATGGATTTGGAATTTGAAAATGGAGTTTGCAGTGACAGACTGGCAA 1312  
 Db 241 TGTGGGATGGATGGATTTGGAATTTGAAAATGGAGTTTGCAGTGACAGACTGGCAA 300  
 QY 1313 ATCCATTGGGATAAGCTCAATTTTGTCTAGG - ATTGGTTCTGATTGGAAGAGCTGCTTTT 1370  
 Db 301 ATCCATTGGGATAAGCTCAATTTTGTCTAGGATTTGTTCTGATTGGAAGAGCTGCTTTT 360  
 QY 1371 GTATTCCCGCTGTGTTTC 1388  
 Db 361 GNAATTCCTGCTGTGTC 378

Search completed: April 5, 2003, 15:54:29  
 Job time : 3725 secs

